

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:42:52 ; Search time 3294 Seconds
(without alignments)
10934.445 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatggcttgcacacctt.....agttcatcaagaagaaaaag 831

Scoring table: OLIGO.NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

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14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

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22: em_ov.*

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29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rtd.*

36: em_hg_nam.*

37: em_hg_vrt.*

38: em_sy.*

39: em_hgo_hum.*

40: em_hgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831	100.0	1594	9	AB002631 Homo sapi
2	831	100.0	1595	6	E29008 Novel colle
3	678	81.6	1016	6	AX376032 Sequence
4	678	81.6	1016	9	AY359038 Homo sapi
5	390	46.9	141262	9	AC080033 Homo sapi
6	390	46.9	141262	2	AC023487 Homo sapi
7	149	17.9	147414	9	AC107953 Homo sapi
8	149	17.9	182475	2	AC023487 Homo sapi
9	63	7.6	767	11	HSU92547
10	35	4.2	234922	2	AC097055 Rattus no
11	28	3.4	867	10	AB016429 Mus muscu
12	28	3.4	166900	2	AC115924 Mus muscu
13	28	3.4	222510	2	AC123656 Mus muscu
14	28	3.4	345420	2	AC131337 Mus muscu
15	26	3.1	231676	2	AC117155 Rattus no
16	26	3.1	231895	2	AC127043 Rattus no
17	26	3.1	239859	2	AC119482 Rattus no
18	26	3.1	241112	2	AC106261 Rattus no
19	26	3.1	258345	2	AC123130 Rattus no
20	23	2.8	151321	2	AC136264 Rattus no
21	22	2.6	1870	8	AF092654 Lycopersi
22	22	2.6	2060	8	AF092655 Lycopersi
23	22	2.6	121112	9	AC124319 Homo sapi
24	22	2.6	163321	2	AC128541 Homo sapi
25	22	2.6	197999	2	AC134688 Homo sapi
26	22	2.6	233566	2	AC118800 Rattus no
27	22	2.6	265067	2	AC097113 Rattus no
28	21	2.5	21	6	E29013 Novel colle
29	21	2.5	21	6	BD096386 Novel sca
30	21	2.5	5909	3	NEMAC24A
31	21	2.5	31812	8	SPUNK4
32	21	2.5	110000	2	EX572105_0
33	21	2.5	110000	2	EX572105_3
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35	21	2.5	151321	2	AC136264 Rattus no
36	21	2.5	161072	9	AL356580 Human DNA
37	21	2.5	161146	10	AC121976 Mus muscu
38	21	2.5	164611	2	AC128858 Rattus no
39	21	2.5	176982	5	AL732610 Zebrafish
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41	21	2.5	206839	2	AC108244 Rattus no
42	21	2.5	216840	2	AC106609 Rattus no
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44	21	2.5	267464	2	AC114904 Mus muscu
45	21	2.5	280815	2	AC107562 Rattus no

ALIGNMENTS

RESULT 1
AB002631
LOCUS Homo sapiens mRNA for collectin 34, complete cds.
DEFINITION
ACCESSION AB002631
VERSION AB002631.1 GI:5162874
KEYWORDS collectin 34
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Yamazaki,H.,
Keshi,H., Sakai,Y., Fukuh,A., Sakamoto,T. and Wakamiya,N.
AUTHORS Molecular cloning of a novel human collectin from liver (CL-L1)

1594 bp mRNA linear PRI 24-JUN-1999

J. Biol. Chem. 274 (19), 13681-13689 (1999)

99240768
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLES
JOURNAL

Submitted (04-APR-1997) Katsuki Ohtani, Osaka Prefectural Institute
of Public Health, Department of Pathology; 3-69, Nakamichi 1-chome
Higashinari-ku, Osaka, Osaka 537, Japan
(E-mail:suzuki@iph.pref.osaka.jp, Tel:+81-6-972-1321,
Fax:+81-6-972-0772)

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polya_signal 1037. .1041

ORIGIN

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Matches 831; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 66 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 125

QY 121 ACACACACAAATTCACAGAGCCCAAGGAGATGATGGTGAAGAAGAGATCCAGGAGAA 180
Db 126 ACACACACAAATTCACAGAGCCCAAGGAGATGATGGTGAAGAAGAGATCCAGGAGAA 185

QY 181 GAGGGAAAGCATGGCAAGTGGGACGCGATGGGGCCGAAAGAGAAATTAAGAGAGAACTGGGT 240
Db 186 GAGGGAAAGCATGGCAAGTGGGACGCGATGGGGCCGAAAGAGAAATTAAGAGAGAACTGGGT 245

QY 241 GATATGGAGATCGGGCAATATTGGACAGATCGGGCCCATTTGGGAAGAAGGGTGACAAA 300
Db 246 GATATGGAGATCGGGCAATATTGGACAGATCGGGCCCATTTGGGAAGAAGGGTGACAAA 305

QY 301 GGGGAAAAAGGTTTGTCTTGGAACTCTGGAGAAAAAGGCAAAAGCAGGACTGTCTGTGAT 360
Db 306 GGGGAAAAAGGTTTGTCTTGGAACTCTGGAGAAAAAGGCAAAAGCAGGACTGTCTGTGAT 365

QY 361 TGTGGAAGATACCGGAAATTTGTTGNCACACTGGATATTAGTATTGCCCGCTCAAGACA 420
Db 366 TGTGGAAGATACCGGAAATTTGTTGNCACACTGGATATTAGTATTGCCCGCTCAAGACA 425

QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATTAGGAAACTCAAGAGAAATTTCTAC 480
Db 426 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATTAGGAAACTCAAGAGAAATTTCTAC 485

QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGATCCCTAACCCATCGCAGGATTCGGGGT 540
Db 486 TACATCGTGCAGGAGAGAGAACTACAGGGATCCCTAACCCATCGCAGGATTCGGGGT 545

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Db 546 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGACTATGTTGCC 605

Db 246 GATATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTGGGAAGAGGGGTGACAAA 305
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Db 366 TGTGGAGATACCGGAATTTGTTGGCACTGGATATTAGTATTAGTATTCGCCGCTCAAGACA 425
Qy 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 480
Db 426 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 485
Qy 481 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 486 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 545
Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCGTCACTATGTTGCC 600
Db 546 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCGTCACTATGTTGCC 605
Qy 601 AAGAGTGCCTCTTTCGGGTGTTCAATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
Db 606 AAGAGTGCCTCTTTCGGGTGTTCAATTTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 665
Qy 661 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
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Qy 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTCTGGCAGATGGAATGACACA 780
Db 726 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTCTGGCAGATGGAATGACACA 785
Qy 781 GAGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 831
Db 786 GAGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 836

RESULT 3
AX376032 1016 bp DNA linear PAT 01-MAR-2002
LOCUS
DEFINITION Sequence 99 from Patent WO0168848.
ACCESSION AX376032
VERSION AX376032.1 GI:19170408
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0168848-A 99 20-SEP-2001;
Genentech, Inc. (US)
LOCATION/Qualifiers
1. 1016
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ORIGIN
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGAATGCTTGCATCCTTCTCGAGAGAACCAATTATCTCTCTGGTACTATTCTT 60
Db 22 ATGAATGCTTGCATCCTTCTCGAGAGAACCAATTATCTCTCTGGTACTATTCTT 81

Qy 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGTGC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTTACCGCTGAAGTCTGTGTGC 141
Qy 121 ACACACACAATTTTCCAGGACCAAGGAGATGATGGTGAAGAGGAGATCCAGGAGAA 180
Db 142 ACACACACAATTTTCCAGGACCAAGGAGATGATGGTGAAGAGGAGATCCAGGAGAA 201
Qy 181 GAGGAAAGCATGGCAAGTGGGACCCATAGGGGCGAAAGGAATTAAGAGAACTGGGT 240
Db 202 GAGGAAAGCATGGCAAGTGGGACCCATAGGGGCGAAAGGAATTAAGAGAACTGGGT 261
Qy 241 GATATGGGAGATCGGGGCAATATTGGCAAGATTTGGCCCATTTGGGAAGAGGAGTGAACA 300
Db 262 GATATGGGAGATCGGGGCAATATTGGCAAGATTTGGCCCATTTGGGAAGAGGAGTGAACA 321
Qy 301 GGGGAAAAAGTTTGTCTTGGGAATCTTGGAGAAAAAGGCAAGAGGATCTCTGTGTGAT 360
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Qy 361 TGTGGAGATACCGGAATTTGTTGGCACTGGATATTAGTATTAGTATTCGCCGCTCAAGACA 420
Db 382 TGTGGAGATACCGGAATTTGTTGGCACTGGATATTAGTATTAGTATTCGCCGCTCAAGACA 441
Qy 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAATCTGAAGAGAAATTTCTAC 501
Qy 481 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCGTCACTATGTTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCGTCACTATGTTGCC 621
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Qy 661 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
Db 682 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
Qy 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTCTGGCAGATGGAATGACACA 801
Qy 781 GAGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCCATCTTACCATGCTACTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 4
AX359038 1016 bp mRNA linear PRI 03-OCT-2003
LOCUS
DEFINITION Homo sapiens clone DN50980 COLEC10 (UNQ366) mRNA, complete cds.
ACCESSION AX359038
VERSION AX359038.1 GI:37183193
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1016)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hase,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,

TITLE					
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P. The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment					
JOURNAL					
PUBLISHED	Genome Res.	13 (10)	2265-2270	(2003)	
REFERENCE					
AUTHORS	Clark,H.F.				
JOURNAL					
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA					
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QY	61	TTGCCAAATTCAGAGTCGGGTCTGGATATTGATAGCGGTCCTACCGCTGAAGTCGTGCCC	120		
Db	82	TTGCCAAATTCAGAGTCGGGTCTGGATATTGATAGCGGTCCTACCGCTGAAGTCGTGCCC	141		
QY	121	ACACACACAATTTCCACAGGACCACCAAGGAGATGATGGTGAAAAGGAGATCCAGAGAA	180		
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QY	181	GAGGAAAAGCATGCCAAGTGGGACGATGGGGCCGAAAAGGAATTAAAGGAGAACTGGGT	240		
Db	202	GAGGAAAAGCATGCCAAGTGGGACGATGGGGCCGAAAAGGAATTAAAGGAGAACTGGGT	261		
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Db	322	GGGGAAAAAGGTTTGTCTTTGGAATACCTGGGAAAAAAGCGAAGCAGGTACTCTCTGTGAT	381		
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QY	481	TACATCGTCGAGGAAGAGAACTACAGGGAATCCCTTAACCCACCTGCAGGATTCGGGGT	540		

Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

4. (bases 1 to 141262)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguski, M., Bouckhagter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, J., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 20, 2002 this sequence version replaced gi:18653568.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L10939

Center clone name: 885_J_16

FEATURES

source

Location/Qualifiers
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1078..1082
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 complement(3941..4471)
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 /rpt_family="L2"
 6439..6500
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 6584..6694
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 6950..7186
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 7187..7549
 /rpt_family="THE1C"
 7217..7221
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 7550..7821
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 complement(9246..9693)
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 9893..10022
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 10245..10649
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 10921..12580
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 14318..14351
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 complement(14623..14738)
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 14892..15130
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 15183..15254
 /rpt_family="MLT1C"
 15276..15710
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unsure

repeat_region

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unsure

unsure

unsure

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complement(19159..19244)

Query Match      46.9%; Score 390; DB 9; Length 141262;
Best Local Similarity 100.0%; Pred. No. 4.4e-207;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTCGAGGAGAGAAG 501
DB 55935 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTCGAGGAGAGAAG 55994
QY 502 AACTACAGGAAATCCTTAACCCACTGCGAGGATTCGGGGTGAATGCTAGCATGCCCAAG 561
DB 55995 AACTACAGGAAATCCTTAACCCACTGCGAGGATTCGGGGTGAATGCTAGCATGCCCAAG 56054
QY 562 GATGAGCTGCCAACACACTCATCGCTGACTATGTTGCCAGAGTGGCTTCTTCGGGTG 621
DB 56055 GATGAGCTGCCAACACACTCATCGCTGACTATGTTGCCAGAGTGGCTTCTTCGGGTG 56114
QY 622 TTCTATGGCGTGAATGACCTTGAAAGGAGGAGACAGTACATGTTTCACAGACAACACTCCA 681
DB 56115 TTCTATGGCGTGAATGACCTTGAAAGGAGGAGACAGTACATGTTTCACAGACAACACTCCA 56174
QY 682 CTGCAGACTATAGCACTGAGTGGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 741
DB 56175 CTGCAGACTATAGCACTGAGTGGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 56234
QY 742 TGTGTGGAGATGCTGAGCTCTGCGAGATGGAAATGACACAGAGTGCCTATCTTACCATGTAC 801
DB 56235 TGTGTGGAGATGCTGAGCTCTGCGAGATGGAAATGACACAGAGTGCCTATCTTACCATGTAC 56294
QY 802 TTGTCTGTGAGTTCATCAAGAGAAAAG 831
DB 56295 TTGTCTGTGAGTTCATCAAGAGAAAAG 56324

RESULT 6
AC023487/c      182475 bp      DNA      linear      HTG 26-MAR-2001
LOCUS      Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
DEFINITION      SEQUENCE, 3 unordered pieces.
ACCESSION      AC023487
VERSION      AC023487.10 GI:13357236
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEPIN.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 182475)
AUTHORS      Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedorov,S., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M.,
Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D.,
Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 182475)
AUTHORS      Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
JOURNAL      Direct Submission
REFERENCE      Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
AUTHORS      Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT      On Mar 16, 2001 this sequence version replaced gi:13324778.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSTDC
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Web site: <http://sequence-www.stanford.edu/group/human/>
Contact: hum-info@sequence.stanford.edu

----- Project Information

Center Project name: 844

Center Clone name: RP11-164H21

----- Summary Statistics

Sequencing Vector: M13mp18; X02513; 98% of reads

Sequencing Vector: plasmid; plasmid_accession; 2% of reads

Chemistry: Dye-primer; 0% of reads

Chemistry: Dye-terminator Big Dye; 99% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 180260 bases at least Q40

Consensus quality: 180441 bases at least Q30

Consensus quality: 180507 bases at least Q20

Insert size: 178514; agarose-fp

Insert size: 182275; sum-of-contigs

Quality coverage: 8.1x in Q20 bases; agarose-fp

Quality coverage: 7.9x in Q20 bases; sum-of-contigs.

NOTE: This is a 'working draft' sequence. It currently

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.

as soon as it is available and the accession number will

be preserved.

1 42072: contig of 42072 bp in length

42073 42172: gap of unknown length

42173 109254: contig of 67082 bp in length

109255 109354: gap of unknown length

109355 182475: contig of 73121 bp in length.

FEATURES

Location/Qualifiers

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109355..182475

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clone_end:SP6"

misc_feature

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109355..182475

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clone_end:SP6"

ORIGIN

Query Match 46.9%; Score 390; DB 2; Length 182475;

Best Local Similarity 100.0%; Pred. No. 4.2e-207;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTCGAGGAGAGAAG 501

DB 6233 GTGATAGCAGGATTAGGAACTGAAGAGAAATTTACTACATCGTCGAGGAGAGAAG 6174

QY 502 AACTACAGGAAATCCTTAACCCACTGCGAGGATTCGGGGTGAATGCTAGCATGCCCAAG 561

DB 6173 AACTACAGGAAATCCTTAACCCACTGCGAGGATTCGGGGTGAATGCTAGCATGCCCAAG 6114

QY 562 GATGAGCTGCCAACACACTCATCGCTGACTATGTTGCCAGAGTGGCTTCTTCGGGTG 621

DB 6113 GATGAGCTGCCAACACACTCATCGCTGACTATGTTGCCAGAGTGGCTTCTTCGGGTG 6054

QY 622 TTCTATGGCGTGAATGACCTTGAAAGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 681

DB 6053 TTCTATGGCGTGAATGACCTTGAAAGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 5994

QY 682 CTGCAGAACTATAGCACTGAGTGGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 741

DB 5993 CTGCAGAACTATAGCACTGAGTGGGAGGAGACCCAGCGACCCCTATGCTCATGAGGAC 5934

QY	742	TGTGTCGGAGATCTGACGCTCTGGCAGATGAANTGACACAGAGTGCATCTTACCATTGAC	801
Db	5933	TGTGTCGGAGATGCTTGACGCTCTGGCAGATGAANTGACACAGAGTGCATCTTACCATTGAC	5874
QY	802	TTTGTCTGTGAGTTCATCAAGAAGAAAAAG	831
Db	5873	TTTGTCTGTGAGTTCATCAAGAAGAAAAAG	5844

RESULT 7	AC107953	147414 bp DNA linear PRI 31-MAR-2002
LOCUS	Homo sapiens chromosome 8, clone RP11-27814, complete sequence.	
DEFINITION		
ACCESSION	AC107953.3 GI:19849383	
VERSION	HTG.	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM		
REFERENCE		
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choquel,Y., Colangelo,M., Collins,S., Collumore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gordon,S., Guyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Hord,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J.J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Menga,V., Murphy,T., Naylor,J.J., Nguyen,C., Nicol.R., Norbu,C., Norman,C.H., O'Connor.T., O'Donnell,P., O'Neil.D., Oliver,J., Peterson,K., Phunkhang.P., Pierre.N., Pollara.V., Raymond.C., Retta.R., Riback.M., Riley.R., Rise,C., Rogov.P., Roman,J., Rosetti,M., Roy.A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer.B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers.M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye.W.J., Young,G., Zainoun,J., Zembek.L., Zimmer,A. and Zody,M.	
JOURNAL	Direct Submission	
REFERENCE	Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
AUTHORS	3 (bases 1 to 147414) Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choquel,Y., Colangelo,M., Collins,S., Collumore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gordon,S., Guyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Hord,L., Hulme,M., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J.J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Menga,V., Murphy,T., Naylor,J.J., Nguyen,C., Nicol.R., Norbu,C., Norman,C.H., O'Connor.T., O'Donnell,P., O'Neil.D., Oliver,J., Peterson,K., Phunkhang.P., Pierre.N., Pollara.V., Raymond.C., Retta.R., Riback.M., Riley.R., Rise,C., Rogov.P., Roman,J., Rosetti,M., Roy.A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer.B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers.M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye.W.J., Young,G., Zainoun,J., Zembek.L., Zimmer,A. and Zody,M.	

[illegible]

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8667..9349
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9884..10022
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repeat_region /rpt_family="L2"
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repeat_region /rpt_family="AT_rich"
11463..11863
repeat_region /rpt_family="LIME3A"
12429..12459
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12744..12790
repeat_region /rpt_family="(TC)n"
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15285..15339
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21748..22031
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complement(24128..24173)
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Best local Similarity 100.0%; Pred. No. 7.2e-72;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATGGCTTTCATCCTTGGCTTCGATATTTGATAGCGTCTACCGTGAAGTCTGTGCC 60
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QY 61 TTGCAAAATTCAGATCTGGGTCTGGATATTTGATAGCGTCTACCGTGAAGTCTGTGCC 120
DB 128565 TTGCAAAATTCAGATCTGGGTCTGGATATTTGATAGCGTCTACCGTGAAGTCTGTGCC 128624
QY 121 ACACACACAATTTCCACGAGCCCAAGG 149
DB 128625 ACACACACAATTTCCACGAGCCCAAGG 128653
RESULT 8
AC023487 182475 bp DNA linear HTG 26-MAR-2001
LOCUS Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT
DEFINITION AC023487
SEQUENCE, 3 unordered pieces.
AC023487
AC023487.10 GI:13357236
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 182475)
AUTHORS Abola.A.P., Bruno.D., Conn.L., Dela Rosa.M., Faulkner.D.,
Federspiel.N., Glukhov.S., Hansen.N., Herman.Z.S., Hyman.R.,
Mac.J., Komp.C., Kottler.S., Lam.B., Marathe.R., Miranda.M.,
Morehouse.A.J., Nguyen.M., Oefner.P., Palm.C.J., Ramirez.D.,
Southwick.A.M., Webb.C., Wilhelmy.J., Yu.S. and Davis.R.W.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 182475)
AUTHORS Bruno.D., Conn.L., Dela Rosa.M., Faulkner.D., Federspiel.N.,
Glukhov.S., Hansen.N., Hyman.R., Mac.J., Marathe.R.,
Morehouse.A.J., Oefner.P., Palm.C.J., Ramirez.D., Wilhelmy.J.,
Yu.S. and Davis.R.W.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT On Mar 16, 2001 this sequence version replaced gi:13324778.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 844
Center clone name: RP11-164H21
----- Summary Statistics
Sequencing Vector: M13mp18; X02513; 98% of reads
Sequencing Vector: plasmid; plasmid_accession; 2% of reads
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 180260 bases at least Q40
Consensus quality: 180441 bases at least Q30
Consensus quality: 180507 bases at least Q20
Insert size: 178614; agarose-fp
Insert size: 182275; sum-of-contigs
Quality coverage: 8.1x in Q20 bases; agarose-fp
Quality coverage: 7.9x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42072: contig of 42072 bp in length
* 42073 42172: gap of unknown length
* 42173 109254: contig of 67082 bp in length
* 109255 109354: gap of unknown length

* 109355 182475: contig of 73121 bp in length.

FEATURES

Location/Qualifiers
1..182475
/organism="Homo sapiens"
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ORIGIN

Query Match 17.9% Score 149; DB 2; Length 182475;

Best Local Similarity 100.0%; Pred. No. 7e-72;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGCTTTGGCATCTCTGCTTTCGAGAAACCAATTATCTCTCTGGTACTATTTCT 60
DB 105635 ATGAATGCTTTGGCATCTCTGCTTTCGAGAAACCAATTATCTCTCTGGTACTATTTCT 105694
QY 61 TTGCAATTCAGATCTGGTCTCGATTTGATAGCGTCTCCGCTGAGCTCTGCTGCTG 120
DB 105695 TTGCAATTCAGATCTGGTCTCGATTTGATAGCGTCTCCGCTGAGCTCTGCTGCTG 105754
QY 121 ACACACACAAATTCACGAGGACCCAAAGG 149
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RESULT 9

HSU92547/c
LOCUS HSU92547 767 bp DNA linear STS 26-OCT-1997
DEFINITION Homo sapiens chromosome 8 STS, sequence tagged site.
ACCESSION U92547
VERSION U92547.1 GI:2564795
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 767)
Pierce, J., Leach, R. and Naylor, S.
New STS markers for human chromosome 8
UNPUBLISHED
2 (bases 1 to 767)
Pierce, J., Leach, R. and Naylor, S.
Direct Submission
Submitted (10-MAR-1997) Pathology, UTHSCSA, 7703 Floyd Curl Drive,
San Antonio, TX 78284, USA
LOCATION/Qualifiers
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FEATURES

Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 405 TGC 407
DB 480 TGC 478

RESULT 10

AC097055 234922 bp DNA linear HTG 15-NOV-2002
LOCUS AC097055
DEFINITION Rattus norvegicus clone CH230-2F22, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC097055
ACCESSION AC097055.5 GI:25007102
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 234922)

REFERENCE

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, P.R., Allen, C.,
Albrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisege, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Svatek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Umani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 234922)

REFERENCE

AUTHORS

Worley, K.C.

Direct Submission

Unpublished

3 (bases 1 to 234922)

REFERENCE

AUTHORS

Worley, K.C.

Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 234922)
Worley, K.C.

TITLE Direct Submission
JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 15, 2002 this sequence version replaced gi:23664540. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: T005
 Center clone name: CH230-2F22
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 231210 bases at least Q40
 Consensus quality: 232236 bases at least Q30
 Consensus quality: 233086 bases at least Q20
 Estimated insert size: 241867; sum-of-contigs estimation
 Quality coverage: 11x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 188689: contig of 188689 bp in length
 * 188690 188789: gap of unknown length
 * 188790 232956: contig of 44167 bp in length
 * 232957 233056: gap of unknown length
 * 233057 234922: contig of 1866 bp in length.

FEATURES Location/Qualifiers
 source
 1..234922
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-2F22"

ORIGIN
 Query Match 4.2%; Score 35; DB 2; Length 234922;
 Best Local Similarity 100.0%; Pred. No. 6.2e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 733 CATGAGGACTGTGGAGACTCTGAGCTCTGGCAG 767
 |||||
 Db 14594 CATGAGGACTGTGGAGACTCTGAGCTCTGGCAG 14628

RESULT 11
 AB016429 867 bp mRNA linear ROD 07-JAN-2003
DEFINITION Mus musculus mRNA for collectin-L1, complete cds.
ACCESSION AB016429
VERSION AB016429.1 GI:27530340
KEYWORDS collectin-L1.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE
 1
AUTHORS Kawai, T., Suzuki, Y., Eda, S., Kase, T., Ohtani, K., Sakai, Y.,
 Keshi, H., Fukuchi, A., Sakamoto, T., Nozaki, M., Copeland, N.G.,
 Jenkins, N.A. and Wakamiya, N.
TITLE Molecular cloning of mouse collectin liver 1
JOURNAL Biosci. Biotechnol. Biochem. 66 (10), 2134-2145 (2002)
MEDLINE 2333927
PUBMED 12450124
REFERENCE 2 (bases 1 to 867)
AUTHORS Kawai, T. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Takao Kawai, Osaka Prefectural Institute of
 Public Health, Laboratory of Food Microbiology; 3-69 Nakamichi
 1-chome, Higashinari-ku, Osaka 537-0025, Japan
 (E-mail:kawai@ph.pref.osaka.jp; Tel:81-6-972-1321,
 Fax:81-6-972-2393)

FEATURES Location/Qualifiers
 source
 1..867
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL 6J"
 /db_xref="taxon:10090"
 /clone="mC11-NIC1-9"
 /tissue_type="liver"
 9..842
 /codon_start=1
 /product="collectin-L1"
 /protein_id="BAC53954.1"
 /db_xref="GI:27530341"
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 SPQKGDGERTGDEEGDKGVKQGPVKVQGLDISVRLKTSKFIKNVIAGIRETEKFFY
 KGLGIHPGKGRAGTICDCGRYKVVQGLDISVRLKTSKFIKNVIAGIRETEKFFY
 YIVCEKNYRESLTHCRIRGGLAMPKDVVNTLIADYVAKSGFRRFVGVNDLREGR
 OYVETDTPQVSNWKEPSPSGHEDCVEMLSGGRWNTDECHLTWVFCFVKKK
 X"

CDS
 Query Match 3.4%; Score 28; DB 10; Length 867;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 GGGAACTGAAGAGAAATCTACTACAT 485
 |||||
 Db 466 GGGAACTGAAGAGAAATCTACTACAT 493

RESULT 12
 AC115924 166900 bp DNA linear HTG 18-JUN-2003
LOCUS Mus musculus clone RP24-511011, WORKING DRAFT SEQUENCE, 4 ordered
DEFINITION pieces.
ACCESSION AC115924
VERSION AC115924.4 GI:31880195
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE
 1 (bases 1 to 166900)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-511011
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166900)
AUTHORS Birren, B., Lincoln, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 166900)

REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagater, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (18-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 18, 2003 this sequence version replaced gi:21490462.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L24895
Center clone name: 511_O_11
----- Summary Statistics
Sequencing vector: Plasmid; N/A; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165673 bases at least Q40
Consensus quality: 166156 bases at least Q30
Consensus quality: 166365 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 166600; sum-of-contigs
Quality coverage: 13.2 in Q20 bases; agarose-fp
Quality coverage: 12.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced

* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 48320: contig of 48320 bp in length
48321 48420: gap of 100 bp
48421 59799: contig of 11379 bp in length
59800 59899: gap of 100 bp
59900 135830: contig of 75931 bp in length
135831 135930: gap of 100 bp
135931 166900: contig of 30970 bp in length.

Location/Qualifiers
1..166900
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-511011"
/clone_lib="RPC1-24 Male Mouse BAC"

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1..48320
/note="assembly_fragment
clone end:SP6
vector_side:left"

misc_feature
48421..59799
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misc_feature
59900..135830
/note="assembly_fragment"

misc_feature
135931..166900
/note="assembly_fragment
clone end:T7
vector_side:right"

ORIGIN
Query Match 3.4%; Score 28; DB 2; Length 166900;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 GCGAACTGAGAGAGAAATCTACTACAT 485
|||||
Db 15164 GCGAACTGAGAGAGAAATCTACTACAT 15191
|||||

RESULT 13
AC123656 222510 bp DNA linear HTG 27-MAR-2003
LOCUS
DEFINITION
Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered pieces.
AC123656
VERSION
AC123656.6 GI:29294284
KEYWORDS
HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 222510)
AUTHORS
Birren, B., Nusbaum, C. and Lander, E.
TITLE
Mus musculus, clone RP23-188M21
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 222510)
AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagater, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

```

* 150362 150461: gap of 100 bp
* 150462 222510: contig of 32049 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP23-188M21"
                     /clone_lib="RP23-188M21"
     misc_feature     1..2031
                     /note="assembly_fragment"
     misc_feature     2132..15244
                     /note="assembly_fragment"
     misc_feature     15345..37649
                     /note="assembly_fragment"
     misc_feature     37750..148102
                     /note="assembly_fragment"
     misc_feature     148203..190361
                     /note="assembly_fragment"
     misc_feature     190462..222510
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN
Query Match          3.4%; Score 28; DB 2; Length 222510;
Best Local Similarity 100.0%; Pred.No. 0.00053;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 GCGAACTGAAGAGAAATTCTACTACAT 485
      |||||
Db 157216 GCGAACTGAAGAGAAATTCTACTACAT 157243

RESULT 14
AC113337
LOCUS
DEFINITION Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered
pieces.
AC113337
VERSION AC113337.4 GI:30017797
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren,B., Nusbaum,C. and Lander,B.
1 (bases 1 to 345420)
Mus musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Canarata,J., Chang,J., Chazaro,B., Choepel,Y., Collumors,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K.P., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gird,S., Graham,L., Grand-Pierre,L., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naytor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rice,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talama,J.,
Tefaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
REFERENCE

```


AUTHORS

Birren, B., Nussbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgaert, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Erickson, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Drakellano, K., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Miho, T., Miho, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL

COMMENT

Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28626850.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WISR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 126504
Center clone name: 480_E_1

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

```

1 1221: contig of 1221 bp in length
* 1222 1321: gap of 100 bp
* 1322 2740: contig of 1419 bp in length
* 2741 2840: gap of 100 bp
* 2841 4351: contig of 1511 bp in length
* 4352 4451: gap of 100 bp
* 4452 7231: contig of 2780 bp in length
* 7232 7331: gap of 100 bp
* 7332 13580: contig of 6249 bp in length
* 13581 13680: gap of 100 bp
* 13681 19224: contig of 5544 bp in length
* 19225 19324: gap of 100 bp
* 19325 24245: contig of 4921 bp in length
* 24246 24345: gap of 100 bp
* 24346 33304: contig of 8959 bp in length
* 33305 34040: gap of 100 bp
* 34041 43959: contig of 10555 bp in length
* 43960 44059: gap of 100 bp
* 44060 64192: contig of 20133 bp in length
* 64193 64292: gap of 100 bp
* 64293 140233: contig of 75941 bp in length
* 140234 140333: gap of 100 bp
* 140334 166937: contig of 26604 bp in length
* 166938 167037: gap of 100 bp
* 167038 202564: contig of 35527 bp in length
* 202565 202664: gap of 100 bp
* 202665 235865: contig of 33201 bp in length
* 235866 282239: contig of 46274 bp in length

```

FEATURES
source

```

* 282240 282339: gap of 100 bp
* 282340 325240: contig of 42901 bp in length
* 325241 325340: gap of 100 bp
* 325341 345420: contig of 20080 bp in length.
Location/Qualifiers
1..345420

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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-480B1"

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/clone_lib="RPC1-23 Female Mouse BAC"
1..1221

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/note="assembly_fragment"
1322..2740

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/note="assembly_fragment"
2841..4351

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```

/note="assembly_fragment"
4452..7231

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7332..13580

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Best Local Similarity 100.0%; Pred.No. 0.00049;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 458 GGGAACTGAAGAGAAATTCCTACTACAT 485
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Db 176241 GGGAACTGAAGAGAAATTCCTACTACAT 176268

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RESULT 15

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AC117155/c
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LOCUS AC117155 231676 bp DNA linear HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-174N22, WORKING DRAFT SEQUENCE, 3
uncloned pieces.

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ACCESSION AC117155
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VERSION AC117155.4 GI:25013203
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KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
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SOURCE Rattus norvegicus (Norway rat)
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ORGANISM

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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

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REFERENCE 1 (bases 1 to 231676)
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AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Ayoagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bardarane, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Eucan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geet, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hayes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulsegad, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwakoelameh, O., Okwuonu, G., Olampunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Flopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quintero, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczyska, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished
2 (bases 1 to 231676)

Worley, K.C.

Direct Submission

Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 231676)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23194714.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GUGP
Center clone name: CH230-174N22

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 220570 bases at least Q40

Consensus quality: 222683 bases at least Q30

Consensus quality: 223867 bases at least Q20

Estimated insert size: 225142; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

* 1 229141: contig of 229141 bp in length

* 229142 229241: gap of unknown length

* 229242 230303: contig of 1062 bp in length

* 230304 230403: gap of unknown length

* 230404 231676: contig of 1273 bp in length.

FEATURES

source

1..231676

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/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clones="CH230-174N22"

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6422..6947

/note="clone boundary"

clone_end:Sp6"

site:

end_sequence:BH350085"

complement(228397..228871)

/note="clone boundary"

clone_end:T7

site:

end_sequence:BH350083"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0069;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 805 GTCGTGAGTTCATCAGAGAGAAAA 830

Db 197764 GTCGTGAGTTCATCAGAGAGAAAA 197739

Search completed: March 11, 2004, 20:30:18

Job time : 3304 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:59:01 ; Search time 396 Seconds
(without alignments)
8914.779 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatgcttgcctcctt.....agttcatcaagaagaaag 831

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	831	100.0	1595	2	AX88323 Human col
2	678	81.6	1016	2	Aaz33973 Human PRO
3	678	81.6	1016	3	Aac78480 Human PRO
4	678	81.6	1016	4	Aas45974 Human DNA
5	678	81.6	1016	7	Abx78577 Human PRO
6	678	81.6	1016	7	ACA75549 Novel hum
7	678	81.6	1016	7	ACA71029 Human sec
8	678	81.6	1016	7	ACC87557 Human sec
9	678	81.6	1016	7	ACC86943 Human sec
10	678	81.6	1016	7	ACD04116 Human sec
11	678	81.6	1016	7	ACA69447 cDNA enco
12	678	81.6	1016	7	ACA90292 Novel hum
13	678	81.6	1016	7	ACC89399 Human sec
14	678	81.6	1016	7	ACA98190 Novel hum
15	678	81.6	1016	7	ACA93832 Human sec
16	678	81.6	1016	7	ACD15225 Human sec
17	678	81.6	1016	7	ACD08812 Human sec
18	678	81.6	1016	7	ACC96732 Human sec
19	678	81.6	1016	7	ACF15453 Human sec
20	678	81.6	1016	7	ACD42506 Novel hum
21	678	81.6	1016	7	ACA72820 Human PRO
22	678	81.6	1016	7	ACD02992 Novel hum
23	678	81.6	1016	7	ACD01807 Novel hum

24	678	81.6	1016	7	ACA91999 Novel hum
25	678	81.6	1016	7	ACA63541 Novel hum
26	678	81.6	1016	7	ACA89424 cDNA enco
27	678	81.6	1016	7	ACA73434 Human sec
28	678	81.6	1016	7	ACA05749 Human sec
29	678	81.6	1016	7	ACA65583 cDNA enco
30	678	81.6	1016	7	ACF20158 Human sec
31	678	81.6	1016	7	ACF19544 Human sec
32	678	81.6	1016	7	ACD21832 Human sec
33	678	81.6	1016	7	ACF12997 Human sec
34	678	81.6	1016	7	ACD25100 Human sec
35	678	81.6	1016	7	ACF00149 Human sec
36	678	81.6	1016	7	ACA72206 Novel hum
37	678	81.6	1016	7	ACD04730 Novel hum
38	678	81.6	1016	7	ACD18191 Human sec
39	678	81.6	1016	7	ACD08198 Human sec
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43	678	81.6	1016	7	ACC74211 Human sec
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ALIGNMENTS

RESULT 1
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ID AX88323 standard; cDNA; 1595 BP.
XX
AC AX88323;
XX
DT 30-SEP-1999 (first entry)
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DE Human collectin cDNA.
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KW Collectin; human; antibacterial; antiviral; treatment; infection; ds.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 6...839
FT /*tag= a
FT /product= "collectin"
XX
PN WO9937767-A1.
XX
PD 29-JUL-1999.
XX
PF 24-JUL-1998; 98WO-JP003328.
XX
PR 23-JAN-1998; 98JP-00011281.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI; 1999-458691/38.
XX
P-PSDB; AAY25518.
XX
PT New collectin protein of human origin and DNA encoding it.
XX
PS Claim 2; Page 39-42; 58pp; Japanese.
XX
CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.
XX
CC This sequence encodes the novel human collectin
XX
SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 U; 0 Other;

Query Match		100.0%; Score 831; DB 2; Length 1595;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 831; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGAAATTCAGAGTCTGGTCTGGATATGATAGCGTCTACCGTCAAGTCTGTGCC
DB	6	ATGAAATTCAGAGTCTGGTCTGGATATGATAGCGTCTACCGTCAAGTCTGTGCC
QY	61	TTGCAAAATTCAGAGTCTGGTCTGGATATGATAGCGTCTACCGTCAAGTCTGTGCC
DB	66	TTGCAAAATTCAGAGTCTGGTCTGGATATGATAGCGTCTACCGTCAAGTCTGTGCC
QY	121	ACACACACAAATTCACAGGACCCAAAGAGATGATAGTGAAGAGATCCAGAGAA
DB	126	ACACACACAAATTCACAGGACCCAAAGAGATGATAGTGAAGAGATCCAGAGAA
QY	181	GAGGGAAGATCGGCAAGTGGGACGATCGGCGGCGGAAAGAAATTAAGGAGAACTGGGT
DB	186	GAGGGAAGATCGGCAAGTGGGACGATCGGCGGCGGAAAGAAATTAAGGAGAACTGGGT
QY	241	GATATGGGAGATCGGGGCAATATGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAA
DB	246	GATATGGGAGATCGGGGCAATATGGCAAGACTGGGCCCATTTGGGAAGAGGTGACAA
QY	301	GGGGAAGAGTTTCTTGGATATCTGGATAGCTGGGAAAGGCAAGCAGTACTGTCTGTAT
DB	306	GGGGAAGAGTTTCTTGGATATCTGGATAGCTGGGAAAGGCAAGCAGTACTGTCTGTAT
QY	361	TGTGGAGATACCGGAATTTGTGGCAACTGAGTATATAGTATGCGCGCTCAAGACA
DB	366	TGTGGAGATACCGGAATTTGTGGCAACTGAGTATATAGTATGCGCGCTCAAGACA
QY	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAGCTGAAGAGAAATTTCTAC
DB	426	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAGCTGAAGAGAAATTTCTAC
QY	481	TACATCGTCGAGAGAGAGAACTACAGGAAATCCCTAACCCACTCGAGATTCGGGGT
DB	486	TACATCGTCGAGAGAGAGAACTACAGGAAATCCCTAACCCACTCGAGATTCGGGGT
QY	541	GGATCTAGCATGCCCAAGATGAAGTCAAGTCAAGCACTCATCGCTGCTATGTGCC
DB	546	GGATCTAGCATGCCCAAGATGAAGTCAAGTCAAGCACTCATCGCTGCTATGTGCC
QY	601	AGAGTGGCTTTCTTGGGTGTTCATTCGGGTGAATGACCTTGAAGAGGAGGACAGTAC
DB	606	AGAGTGGCTTTCTTGGGTGTTCATTCGGGTGAATGACCTTGAAGAGGAGGACAGTAC
QY	661	ATGTTACAGACAACTCCACTGAGAGTATAGCACTATAGCACTGGAATGAGGGGACCCAGC
DB	666	ATGTTACAGACAACTCCACTGAGAGTATAGCACTATAGCACTGGAATGAGGGGACCCAGC
QY	721	GACCCCTATGGTCAAGAGTGTGTGGAGATGCTGAGCTTGGCAGATGGAATGACACA
DB	726	GACCCCTATGGTCAAGAGTGTGTGGAGATGCTGAGCTTGGCAGATGGAATGACACA
QY	781	GAGTGCATCTACCATGATCTCTGTTGATGATCATCAAGAGAAAG 831
DB	786	GAGTGCATCTACCATGATCTCTGTTGATGATCATCAAGAGAAAG 836

RESULT 2
AAZ33973
ID AAZ33973 standard; cDNA; 1016 BP.
XX AC AAZ33973;
XX DT 07-DEC-1999 (first entry)
XX DX Human PR0702 nucleotide sequence.
XX DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW

KW	secreted protein; transmembrane protein; ss.
XX	Homo sapiens.
OS	WO9946281-A2.
PN	16-SEP-1999.
XX	08-MAR-1999;
PF	99WO-US005028.
XX	10-MAR-1998;
PR	98US-0077450P.
PR	11-MAR-1998;
PR	98US-0077632P.
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PR	98US-0077641P.
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PR	98US-0077649P.
PR	12-MAR-1998;
PR	98US-0077791P.
PR	13-MAR-1998;
PR	98US-0078004P.
PR	17-MAR-1998;
PR	98US-00040220.
PR	20-MAR-1998;
PR	98US-0078886P.
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PR	98US-0078936P.
PR	20-MAR-1998;
PR	98US-0078939P.
PR	25-MAR-1998;
PR	98US-0079294P.
PR	26-MAR-1998;
PR	98US-0079656P.
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PR	98US-0079786P.
PR	30-MAR-1998;
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PR	98US-0079923P.
PR	31-MAR-1998;
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PR	31-MAR-1998;
PR	98US-0080107P.
PR	31-MAR-1998;
PR	98US-0080165P.
PR	31-MAR-1998;
PR	98US-0080194P.
PR	01-APR-1998;
PR	98US-0080327P.
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PR	98US-0080328P.
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PR	98US-0080334P.
PR	08-APR-1998;
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PR	08-APR-1998;
PR	98US-0081070P.
PR	08-APR-1998;
PR	98US-0081071P.
PR	09-APR-1998;
PR	98US-0081195P.
PR	09-APR-1998;
PR	98US-0081203P.
PR	09-APR-1998;
PR	98US-0081229P.
PR	15-APR-1998;
PR	98US-0081817P.
PR	15-APR-1998;
PR	98US-0081838P.
PR	15-APR-1998;
PR	98US-0081952P.
PR	15-APR-1998;
PR	98US-0081955P.
PR	21-APR-1998;
PR	98US-0082568P.
PR	21-APR-1998;
PR	98US-0082569P.
PR	22-APR-1998;
PR	98US-0082700P.
PR	22-APR-1998;
PR	98US-0082704P.
PR	22-APR-1998;
PR	98US-0082804P.
PR	23-APR-1998;
PR	98US-0082767P.
PR	23-APR-1998;
PR	98US-0082796P.
PR	27-APR-1998;
PR	98US-0083336P.
PR	28-APR-1998;
PR	98US-0083322P.
PR	29-APR-1998;
PR	98US-0083392P.
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PR	98US-0083495P.
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PR	29-APR-1998;
PR	98US-0083499P.
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PR	29-APR-1998;
PR	98US-0083559P.
PR	30-APR-1998;
PR	98US-0083742P.
PR	05-MAY-1998;
PR	98US-0084366P.
PR	06-MAY-1998;
PR	98US-0084414P.
PR	06-MAY-1998;
PR	98US-0084441P.
PR	07-MAY-1998;
PR	98US-0084598P.
PR	07-MAY-1998;
PR	98US-0084600P.
PR	07-MAY-1998;
PR	98US-0084627P.

PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AV, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR P-PSDB; AAB44254.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 2; Fig 36; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78500 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
Query Match 81.6%; Score 678; DB 3; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGATGCTTTCATCTTCTGCTTCCAGAACCAATTTATCTCTCTGCTACTATTTCTT 60
DB 22 ATGATGCTTTCATCTTCTGCTTCCAGAACCAATTTATCTCTCTGCTACTATTTCTT 81
QY 61 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTCAAGTCTGTGCC 120
DB 82 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTCAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCAGAGCCCAAGAGAGATGATGCTGAAAGAGATCCAGGAA 180
DB 142 ACACACAAATTTCCAGAGCCCAAGAGAGATGATGCTGAAAGAGATCCAGGAA 201
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DB 802 GAGTGGCATCTTACCATGCTACTTTGTTCTGTGAGTTCATCAGAGAAAG 852
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DT 18-DEC-2001 (first entry)
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KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
FN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
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PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
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PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
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PR 29-MAR-2000; 2000US-0193032P.
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 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 05-JUN-2000; 2000US-0209832P.
 28-JUL-2000; 2000WO-US020710.
 22-AUG-2000; 2000US-00644848.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 (GETH) GENENTECH INC.
 Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 P-PSDB; AAU29073.
 WPI; 2001-602746/68.
 P-PSDB; AAU29073.
 Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 presence of tumors, such as prostate and breast tumors, in mammals and to
 screen for modulators of the compounds.
 Claim 2; Fig 99; 774pp; English.
 Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 primers for PRO polypeptides of the invention. The sequences of the
 invention can be used to detect the presence of a tumour in a mammal by
 comparing the level of expression of a PRO polypeptide in a test sample
 of cells from the animal and a control sample of normal cells, whereby a
 higher level of expression in the test sample indicates the presence of a
 tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 pigs, goats and rabbits but are preferably human. The polypeptides can be
 used to stimulate tumour necrosis factor (TNF) alpha release from human
 blood, when contacted with it. A specific polypeptide can be used to
 stimulate the proliferation or differentiation of chondrocyte cells. The
 PRO proteins can be used to determine the presence of tumours and also
 susceptibility to tumour development, particularly adrenal, lung, colon,
 breast, prostate, rectal, cervical, or liver tumours, in mammalian
 subjects. The oligonucleotide probes specific for the PRO nucleic acids
 can be used for genetic analysis of individuals with genetic disorders
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 QY 481 TACATCGTGGAGAGAGAGAACTACAGGGAATCCCTAACCCACTCCAGGATTCGGGGT 540
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 QY 781 GAGTGCCATCTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAG 831
 Db 802 GAGTGCCATCTTACCATGCTACTTTGCTGTGAGTTTCATCAAGAGAAAG 852
 RESULT 5
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 AC ABX78577;
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 DT 15-APR-2003 (first entry)
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 XX Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
 KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEFT;
 XX antibody-dependent enzyme mediated prodrug therapy.
 OS Homo sapiens.
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 XX US2003027272-A1.
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 XX 06-FEB-2003.
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 XX 21-JUN-2002; 2002US-00176492.
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PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102457P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.

Query Match 81.6%; Score 578; DB 7; Length 1016;

Best Local Similarity 99.6%; Pred.No. 0;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGCTTTTCATCTCTTCGGAAGAAACCAATTTATCTCTGGTACTATTTCTT 60
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Db	22	ATGATGGCTTTGCAATCTTGGTTCGAAGAAACCAATTTATCTCCCTGGTACTATTTCTT	81	PD	13-FEB-2003.
Qy	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCCTCTACCGTCTGAAGTCTGTGCC	120	XX	21-JUN-2002; 2002US-00176756.
Db	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCCTCTACCGTCTGAAGTCTGTGCC	141	XX	
Qy	121	ACACACAAATTCACAGGACCCAAAGAGATGATGTGAAAGAGAGATCCAGGAGAA	180	PR	18-SEP-1997; 97US-0059263P.
Db	142	ACACACAAATTCACAGGACCCAAAGAGATGATGTGAAAGAGAGATCCAGGAGAA	201	PR	18-SEP-1997; 97US-0059266P.
Qy	181	GAGGAAAGATCGGCAAAAGTGGGACCGCATGGGGCCGAAAGAAATTAAGAGAGAACTGGGT	240	PR	17-OCT-1997; 97US-0062250P.
Db	202	GAGGAAAGATCGGCAAAAGTGGGACCGCATGGGGCCGAAAGAAATTAAGAGAGAACTGGGT	261	PR	21-OCT-1997; 97US-0063486P.
Qy	241	GATATGGGAGATCGGGGCAATATTGCGAAGACTGGGCCCATTTGGGAAGAGAGGTTGACAAA	300	PR	24-OCT-1997; 97US-0063120P.
Db	262	GATATGGGAGATCGGGGCAATATTGCGAAGACTGGGGCCCATTTGGGAAGAGAGGTTGACAAA	321	PR	24-OCT-1997; 97US-0063121P.
Qy	301	CGGGAAAAGGTTTCTTGGAACTCTGAGAAAGGCAAGCAGGTACTGTCTGTGAT	360	PR	28-OCT-1997; 97US-0063540P.
Db	322	GGGAAAAGGTTTCTTGGAACTCTGAGAAAGGCAAGCAGGTACTGTCTGTGAT	381	PR	28-OCT-1997; 97US-0063541P.
Qy	361	TGTGAAGATACCGGAAATTTGTTGGAACAATGGATATTAGTATTCGCCCGCTCAAGACA	420	PR	28-OCT-1997; 97US-0063544P.
Db	382	TGTGAAGATACCGGAAATTTGTTGGAACAATGGATATTAGTATTCGCCCGCTCAAGACA	441	PR	28-OCT-1997; 97US-0063564P.
Qy	421	TCTATGAAGTTTGTCAAGATCTGTATGACGGATTAGGGAACCTGAAGAGAAATTTCTAC	480	PR	29-OCT-1997; 97US-0063734P.
Db	442	TCTATGAAGTTTGTCAAGATCTGTATGACGGATTAGGGAACCTGAAGAGAAATTTCTAC	501	PR	31-OCT-1997; 97US-0063870P.
Qy	481	TATCATGTGACAGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTTCGGGT	540	PR	31-OCT-1997; 97US-0064103P.
Db	502	TATCATGTGACAGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTTCGGGT	561	PR	13-NOV-1997; 97US-0065311P.
Qy	541	GGAAATGCTAGCCATGCCCAAGATGAAGTCCCAACACATCATCTGCTGATGTGCC	600	PR	21-NOV-1997; 97US-0066120P.
Db	562	GGAAATGCTAGCCATGCCCAAGATGAAGTCCCAACACATCATCTGCTGATGTGCC	621	PR	24-NOV-1997; 97US-0066466P.
Qy	601	AAGAGTGGCTTCTTTTCGGGTGTTTCATTCGGCTGATGACCTTGAAGGGAGGACAGTAC	660	PR	11-DEC-1997; 97US-0069335P.
Db	622	AAGAGTGGCTTCTTTTCGGGTGTTTCATTCGGCTGATGACCTTGAAGGGAGGACAGTAC	681	PR	12-DEC-1997; 97US-0069425P.
Qy	661	ATGTTCAAGACAACTCCACTGACAGAACTATAGCACTGGAATAGGGGGGAAACCCAGC	720	PR	17-DEC-1997; 97US-0069870P.
Db	682	ATGTTCAAGACAACTCCACTGACAGAACTATAGCACTGGAATAGGGGGGAAACCCAGC	741	PR	18-DEC-1997; 97US-0068017P.
Qy	721	GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCGCATGGAATGACACA	780	PR	10-MAR-1998; 98US-0077450P.
Db	742	GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCGCATGGAATGACACA	801	PR	11-MAR-1998; 98US-0077632P.
Qy	781	GAGTGCCATCTTACCATGCTACTTTGTTGAGTTTCATCAAGAGAAAAAG	831	PR	11-MAR-1998; 98US-0077649P.
Db	802	GAGTGCCATCTTACCATGCTACTTTGTTGAGTTTCATCAAGAGAAAAAG	852	PR	20-MAR-1998; 98US-0078886P.
RESULT 7					20-MAR-1998; 98US-0078939P.
ACAV1029					27-MAR-1998; 98US-0079664P.
ID	ACAV1029 standard; cDNA; 1016 BP.				31-MAR-1998; 98US-0080107P.
XX					31-MAR-1998; 98US-0080194P.
AC					01-APR-1998; 98US-0080327P.
XX					01-APR-1998; 98US-0080333P.
AC					08-APR-1998; 98US-0081049P.
XX					08-APR-1998; 98US-0081070P.
AC					09-APR-1998; 98US-0081195P.
XX					15-APR-1998; 98US-0081838P.
AC					21-APR-1998; 98US-0082568P.
XX					21-APR-1998; 98US-0082569P.
AC					22-APR-1998; 98US-0082704P.
XX					22-APR-1998; 98US-0082797P.
AC					28-APR-1998; 98US-0083322P.
XX					29-APR-1998; 98US-0083495P.
AC					29-APR-1998; 98US-0083496P.
XX					29-APR-1998; 98US-0083499P.
AC					29-APR-1998; 98US-0083559P.
XX					05-MAY-1998; 98US-0084366P.
AC					06-MAY-1998; 98US-0084414P.
XX					07-MAY-1998; 98US-0084639P.
AC					07-MAY-1998; 98US-0084640P.
XX					07-MAY-1998; 98US-0084643P.
AC					15-MAY-1998; 98US-0085579P.
XX					15-MAY-1998; 98US-0085580P.
AC					15-MAY-1998; 98US-0085582P.
XX					15-MAY-1998; 98US-0085700P.
AC					18-MAY-1998; 98US-0086023P.
XX					22-MAY-1998; 98US-0086392P.
AC					22-MAY-1998; 98US-0086486P.
XX					28-MAY-1998; 98US-0087098P.
AC					28-MAY-1998; 98US-0087208P.
XX					02-JUN-1998; 98US-0087609P.
AC					02-JUN-1998; 98US-0087759P.
XX					03-JUN-1998; 98US-0087827P.
AC					04-JUN-1998; 98US-0088025P.
XX					04-JUN-1998; 98US-0088028P.
AC					04-JUN-1998; 98US-0088029P.
XX					04-JUN-1998; 98US-0088033P.
AC					04-JUN-1998; 98US-0088326P.
XX					05-JUN-1998; 98US-0088167P.
AC					05-JUN-1998; 98US-0088202P.

Human secreted/transmembrane protein (PRO) cDNA #50.

Human; Gene; ss; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing.

Homo sapiens.

US2003032112-A1.

PR 05-JUN-1998; 98US-00882122P.
PR 05-JUN-1998; 98US-00882172P.
PR 09-JUN-1998; 98US-00886552P.
PR 10-JUN-1998; 98US-00887222P.
PR 10-JUN-1998; 98US-00887332P.
PR 10-JUN-1998; 98US-00887402P.
PR 10-JUN-1998; 98US-00888112P.
PR 10-JUN-1998; 98US-00888222P.
PR 10-JUN-1998; 98US-00888252P.
PR 10-JUN-1998; 98US-00888262P.
PR 11-JUN-1998; 98US-00888612P.
PR 11-JUN-1998; 98US-00888622P.
PR 11-JUN-1998; 98US-00888762P.
PR 12-JUN-1998; 98US-00890902P.
PR 12-JUN-1998; 98US-00891052P.
PR 16-JUN-1998; 98US-00895112P.
PR 16-JUN-1998; 98US-00895142P.
PR 17-JUN-1998; 98US-00895382P.
PR 17-JUN-1998; 98US-00895982P.
PR 17-JUN-1998; 98US-00896532P.
PR 18-JUN-1998; 98US-00899082P.
PR 18-JUN-1998; 98US-00899522P.
PR 22-JUN-1998; 98US-00902462P.
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PR 24-JUN-1998; 98US-00902542P.
PR 24-JUN-1998; 98US-00904332P.
PR 24-JUN-1998; 98US-00904442P.
PR 24-JUN-1998; 98US-00904612P.
PR 24-JUN-1998; 98US-00905352P.
PR 24-JUN-1998; 98US-00905402P.
PR 25-JUN-1998; 98US-00906762P.
PR 25-JUN-1998; 98US-00906782P.
PR 25-JUN-1998; 98US-00906882P.
PR 25-JUN-1998; 98US-00906902P.
PR 25-JUN-1998; 98US-00906942P.
PR 25-JUN-1998; 98US-00906952P.
PR 25-JUN-1998; 98US-00906962P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-00908622P.
PR 26-JUN-1998; 98US-00908632P.
PR 26-JUN-1998; 98US-00910102P.
PR 01-JUL-1998; 98US-00913592P.
PR 01-JUL-1998; 98US-00915442P.
PR 02-JUL-1998; 98US-00914782P.
PR 02-JUL-1998; 98US-00914862P.
PR 02-JUL-1998; 98US-00916262P.
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PR 02-JUL-1998; 98US-00916322P.
PR 24-JUL-1998; 98US-00940062P.
PR 04-AUG-1998; 98US-00952822P.
PR 10-AUG-1998; 98US-0095982P.
PR 10-AUG-1998; 98US-00960122P.
PR 17-AUG-1998; 98US-00967572P.
PR 17-AUG-1998; 98US-00967662P.
PR 17-AUG-1998; 98US-00968672P.
PR 17-AUG-1998; 98US-00968942P.
PR 17-AUG-1998; 98US-00968972P.
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PR 26-AUG-1998; 98US-00979522P.
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PR 26-AUG-1998; 98US-00979742P.
PR 26-AUG-1998; 98US-00980142P.
PR 01-SEP-1998; 98US-00987162P.
PR 01-SEP-1998; 98US-00987232P.
PR 02-SEP-1998; 98US-00988032P.
PR 02-SEP-1998; 98US-00988212P.
PR 02-SEP-1998; 98US-00988432P.
PR 09-SEP-1998; 98US-00996022P.

PR 10-SEP-1998; 98US-00997412P.
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PR 10-SEP-1998; 98US-00997632P.
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PR 15-SEP-1998; 98US-01003882P.
PR 16-SEP-1998; 98US-01006622P.
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PR 16-SEP-1998; 98US-01017512P.
PR 16-SEP-1998; 98WQ-US019330.
PR 17-SEP-1998; 98US-01006832P.
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PR 17-SEP-1998; 98US-01009192P.
PR 17-SEP-1998; 98US-01009302P.
PR 18-SEP-1998; 98US-01008492P.
PR 18-SEP-1998; 98US-01010142P.
PR 23-SEP-1998; 98US-01010682P.
PR 23-SEP-1998; 98US-01014712P.
PR 23-SEP-1998; 98US-01014722P.
PR 23-SEP-1998; 98US-01014752P.
PR 23-SEP-1998; 98US-01014772P.
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PR 24-SEP-1998; 98US-01017392P.
PR 24-SEP-1998; 98US-01017432P.
PR 25-SEP-1998; 98US-01019222P.
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PR 29-SEP-1998; 98US-0102072P.
PR 29-SEP-1998; 98US-01022402P.
PR 29-SEP-1998; 98US-01023302P.
PR 29-SEP-1998; 98US-01023312P.
PR 30-SEP-1998; 98US-01024872P.
PR 30-SEP-1998; 98US-01025702P.
PR 01-OCT-1998; 98US-01025712P.
PR 01-OCT-1998; 98US-01026842P.
PR 01-OCT-1998; 98US-01026872P.
PR 02-OCT-1998; 98US-01029652P.
PR 06-OCT-1998; 98US-01032582P.
PR 06-OCT-1998; 98US-01034492P.
PR 07-OCT-1998; 98US-00168978.

Query Match 81.6%; Score 678; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGGCATCCTTGCTTCGAAGAAACCAATTTATCCTCTCTGTACTATTCTT 60
DB 22 ATGAATGGCTTTGGCATCCTTGCTTCGAAGAAACCAATTTATCCTCTCTGTACTATTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCCTACCGCTCAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCAGAGCCCAAGGAGATGTTGTAAGAAAGGAGATCCAGGAGAA 180
DB 142 ACACACAAATTTCCAGAGCCCAAGGAGATGTTGTAAGAAAGGAGATCCAGGAGAA 201
QY 191 GAGGGAAGCATGCGCAAGTGGGACGCGATGGGCCGCAAGAGGAATTAAGAGAGAACTGGGT 240
DB 202 GAGGGAAGCATGCGCAAGTGGGACGCGATGGGCCGCAAGAGGAATTAAGAGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAA 300
DB 262 GATATGGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGGTGACAA 321
QY 301 GGGGAAAAGGTTTGGTTGGAATACCTGGGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 322 GGGGAAAAGGTTTGGTTGGAATACCTGGGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTGTTGGACAACTGATATTAGTATTCGCCGCTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTTGGACAACTGATATTAGTATTCGCCGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAACCTCAAGAGAAATTTCTAC 480

Db	442	TCATGAAGTTTGTCAAGAATGTGATAGCAGGAGATTAGGAAACTGAAGAGAAATTCCTAC	501	PR	18-DEC-1997;	97US-0068017P.
Qy	481	ATCATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	540	PR	10-MAR-1998;	98US-0077450P.
Db	502	TACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	561	PR	11-MAR-1998;	98US-0077632P.
Qy	541	GGAATGCTAGCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC	600	PR	20-MAR-1998;	98US-0078886P.
Db	562	GGAATGCTAGCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGCC	621	PR	20-MAR-1998;	98US-0078939P.
Qy	601	AAGAGTGCCTTTTCGGGTTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC	660	PR	27-MAR-1998;	98US-0079564P.
Db	622	AAGAGTGCCTTTTCGGGTTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC	681	PR	27-MAR-1998;	98US-0079786P.
Qy	661	ATGTTTCAGACACACACTCCACTGCAGACTATAGCACTTGAATGAGGGGAGCCACG	720	PR	31-MAR-1998;	98US-0080107P.
Db	682	ATGTTTCAGACACACACTCCACTGCAGACTATAGCACTTGAATGAGGGGAGCCACG	741	PR	31-MAR-1998;	98US-0080194P.
Qy	721	GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA	780	PR	01-APR-1998;	98US-0080327P.
Db	742	GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA	801	PR	01-APR-1998;	98US-0080333P.
Qy	781	GAGTGCATCTTACATGCTACTTTGCTGTGAGTTCTATCAAGAGAAAAG	831	PR	08-APR-1998;	98US-0081049P.
Db	802	GAGTGCATCTTACATGCTACTTTGCTGTGAGTTCTATCAAGAGAAAAG	852	PR	08-APR-1998;	98US-0081070P.
RESULT 8						
ID	ACC87557	standard; cDNA; 1016 BP.		PR	09-APR-1998;	98US-0081195P.
AC	ACC87557;			PR	15-APR-1998;	98US-0081838P.
DT	05-AUG-2003	(first entry)		PR	21-APR-1998;	98US-0082568P.
DE	Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.			PR	21-APR-1998;	98US-0082569P.
KW	Human; PRO; secreted protein; transmembrane protein;			PR	22-APR-1998;	98US-0082704P.
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;			PR	22-APR-1998;	98US-0082797P.
KW	chondrocyte; proliferation; differentiation; cartilage disorder;			PR	28-APR-1998;	98US-0083322P.
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;			PR	29-APR-1998;	98US-0083495P.
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;			PR	29-APR-1998;	98US-0083496P.
KW	liver; drug screening; transgenic animal; genetic analysis;			PR	29-APR-1998;	98US-0083499P.
KW	antiarthritic; vulnery; gene therapy; gene; ss.			PR	05-MAY-1998;	98US-0084366P.
CS	Homo sapiens.			PR	06-MAY-1998;	98US-0084414P.
PN	US2003027278-A1.			PR	07-MAY-1998;	98US-0084639P.
PD	06-FEB-2003.			PR	07-MAY-1998;	98US-0084643P.
PF	21-JUN-2002; 2002US-00176987.			PR	15-MAY-1998;	98US-0085579P.
XX	18-SEP-1997; 97US-0059263P.			PR	15-MAY-1998;	98US-0085580P.
PR	17-OCT-1997; 97US-0059266P.			PR	15-MAY-1998;	98US-0085582P.
PR	21-OCT-1997; 97US-0063486P.			PR	15-MAY-1998;	98US-0085700P.
PR	24-OCT-1997; 97US-0063120P.			PR	18-MAY-1998;	98US-0086023P.
PR	28-OCT-1997; 97US-0063540P.			PR	22-MAY-1998;	98US-0086392P.
PR	28-OCT-1997; 97US-0063541P.			PR	22-MAY-1998;	98US-0086486P.
PR	28-OCT-1997; 97US-0063544P.			PR	28-MAY-1998;	98US-0087098P.
PR	29-OCT-1997; 97US-0063564P.			PR	28-MAY-1998;	98US-0087208P.
PR	31-OCT-1997; 97US-0063734P.			PR	02-JUN-1998;	98US-0087609P.
PR	13-NOV-1997; 97US-0065311P.			PR	03-JUN-1998;	98US-0087759P.
PR	21-NOV-1997; 97US-0066120P.			PR	04-JUN-1998;	98US-0088025P.
PR	24-NOV-1997; 97US-0066466P.			PR	04-JUN-1998;	98US-0088028P.
PR	11-DEC-1997; 97US-0066772P.			PR	04-JUN-1998;	98US-0088029P.
PR	12-DEC-1997; 97US-0069335P.			PR	04-JUN-1998;	98US-0088033P.
PR	17-DEC-1997; 97US-0069870P.			PR	04-JUN-1998;	98US-0088326P.
PR	18-SEP-1997; 97US-0059263P.			PR	05-JUN-1998;	98US-0088167P.
PR	17-OCT-1997; 97US-0059266P.			PR	05-JUN-1998;	98US-0088202P.
PR	21-OCT-1997; 97US-0063486P.			PR	05-JUN-1998;	98US-0088212P.
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PR	28-OCT-1997; 97US-0063544P.			PR	10-JUN-1998;	98US-0088738P.
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PR	13-NOV-1997; 97US-0065311P.			PR	10-JUN-1998;	98US-0088824P.
PR	21-NOV-1997; 97US-0066120P.			PR	10-JUN-1998;	98US-0088825P.
PR	24-NOV-1997; 97US-0066466P.			PR	10-JUN-1998;	98US-0088826P.
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PR	12-DEC-1997; 97US-0069335P.			PR	11-JUN-1998;	98US-0088863P.
PR	17-DEC-1997; 97US-0069870P.			PR	12-JUN-1998;	98US-0088876P.
PR	18-SEP-1997; 97US-0059263P.			PR	12-JUN-1998;	98US-0089090P.
PR	17-OCT-1997; 97US-0059266P.			PR	12-JUN-1998;	98US-0089105P.
PR	21-OCT-1997; 97US-0063486P.			PR	16-JUN-1998;	98US-0089512P.
PR	24-OCT-1997; 97US-0063120P.			PR	16-JUN-1998;	98US-0089514P.
PR	28-OCT-1997; 97US-0063540P.			PR	17-JUN-1998;	98US-0089538P.
PR	28-OCT-1997; 97US-0063541P.			PR	17-JUN-1998;	98US-0089539P.
PR	29-OCT-1997; 97US-0063564P.			PR	17-JUN-1998;	98US-0089588P.
PR	31-OCT-1997; 97US-0063734P.			PR	18-JUN-1998;	98US-0089653P.
PR	13-NOV-1997; 97US-0065311P.			PR	18-JUN-1998;	98US-0089908P.
PR	21-NOV-1997; 97US-0066120P.			PR	19-JUN-1998;	98US-0089952P.
PR	24-NOV-1997; 97US-0066466P.			PR	22-JUN-1998;	98US-0090246P.
PR	11-DEC-1997; 97US-0066772P.			PR	22-JUN-1998;	98US-0090252P.
PR	12-DEC-1997; 97US-0069335P.			PR	22-JUN-1998;	98US-0090252P.
PR	17-DEC-1997; 97US-0069870P.			PR	22-JUN-1998;	98US-0090252P.

PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
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PR 26-JUN-1998; 98US-0091010P.
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PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
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PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091629P.
PR 02-JUL-1998; 98US-0091632P.
PR 24-JUL-1998; 98US-0094004P.
PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
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PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097971P.
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PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 02-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 15-SEP-1998; 98US-0100388P.
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PR 16-SEP-1998; 98US-0101751P.
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PR 17-SEP-1998; 98US-0100930P.
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PR 18-SEP-1998; 98US-0101014P.
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PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.

PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 81.6%; Score 678; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTGATCCTTCTTGAAGAAACCAATTTATCCTCTCTGTACTATTCTT 60
DB 22 ATGAATGGCTTTTGATCCTTCTTGAAGAAACCAATTTATCCTCTCTGTACTATTCTT 81

QY 61 TTGCAATTCAGAGTCGGCTCTGGATTTGATAGCGCTTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAATTCAGAGTCGGCTCTGGATTTGATAGCGCTTACCGCTGAAGTCTGTGCC 141

QY 121 ACACACACAATTTCCACGAGCACCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
DB 142 ACACACACAATTTCCACGAGCACCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGCAAAAGTGGACCGCATGGGCCGGAAGAGATTTAAAGAGACTGGGT 240
DB 202 GAGGAAAGCATGCAAAAGTGGACCGCATGGGCCGGAAGAGATTTAAAGAGACTGGGT 261

QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 300
DB 262 CATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 321

QY 301 GGGGAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTAT 360
DB 322 GGGGAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTAT 381

QY 361 TGTGGAAGATACCGGAAATTTGTGGACAACTGGATATTAGTATTGCCGGGTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTGGACAACTGGATATTAGTATTGCCGGGTCAAGACA 441

QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGAGGATTTAGGAAACTGAAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGAGGATTTAGGAAACTGAAGAAATTTCTAC 501

QY 481 TACATCGTCAGGAAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
DB 502 TACATCGTCAGGAAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561

QY 541 GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTCATCTATGTGTGC 600
DB 562 GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTCATCTATGTGTGC 621

QY 601 RAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTCAAGAGGAGGACAGTAC 660
DB 622 RAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTCAAGAGGAGGACAGTAC 681

QY 661 ATGTTTCAAGACAACTCCACTCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
DB 682 ATGTTTCAAGACAACTCCACTCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741

QY 721 GACCCCTATGGTCATGAGGATGTGTGAGATGTGAGCTCTGCAGATGGAATGACACA 780
DB 742 GACCCCTATGGTCATGAGGATGTGTGAGATGTGAGCTCTGCAGATGGAATGACACA 801

QY 781 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAGAAAG 831
DB 802 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAGAAAG 852

PR	10-AUG-1998;	98US-0096012P.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
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Db	202	GAGGGAAGCATGCGCAAGTGGGACGCGCATGGGCCGGAAGGAATTAAGGAGAACTGGGT 261
QY	241	GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGCTGACAA 300
Db	262	GATATGGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGCTGACAA 321
QY	301	GGGGAAGAGGTTTGGCTTGGAACTCTGGAGAAAGGCAAGCAGGCTACTGCTGTAT 360
Db	322	GGGGAAGAGGTTTGGCTTGGAACTCTGGAGAAAGGCAAGCAGGCTACTGCTGTAT 381
QY	361	TGTGAAGATACCCGAAATTTGTTGCAAACTGGATATTAGTATTGCCCGGCTCAAGACA 420
Db	382	TGTGAAGATACCCGAAATTTGTTGCAAACTGGATATTAGTATTGCCCGGCTCAAGACA 441
QY	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAACCTGAAGAAATTTCTAC 480
Db	442	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAACCTGAAGAAATTTCTAC 501
QY	481	TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCTTAACCCACTGCAGGATTCGGGT 540
Db	502	TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCTTAACCCACTGCAGGATTCGGGT 561
QY	541	GGAATGTAGCCATGCCCCAAGGATGAAGTGCACACACTATCTGCTGACTATGTTGCC 600
Db	562	GGAATGTAGCCATGCCCCAAGGATGAAGTGCACACACTATCTGCTGACTATGTTGCC 621
QY	601	AAGAGTGGCTTCTTTGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 660
Db	622	AAGAGTGGCTTCTTTGGGTGTTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 681
QY	661	ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
Db	682	ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
QY	721	GACCCCTATGTCATGAGGACTGTGAGAGATCTGAGCTCTGGCAGATGGAATGACACA 780
Db	742	GACCCCTATGTCATGAGGACTGTGAGAGATCTGAGCTCTGGCAGATGGAATGACACA 801
QY	781	GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 831
Db	802	GAGTGCCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 852
RESULT 10		
ACD04116		
ID	ACD04116	standard; cDNA; 1016 BP.
XX	AC	ACD04116;
XX	AC	ACD04116;
DT	09-AUG-2003	(first entry)
XX	DE	Human secreted/transmembrane protein (PRO) cDNA #50.
XX	DE	Human secreted/transmembrane protein (PRO) cDNA #50.
KW	KW	Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
KW	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW	KW	tissue typing.
OS	OS	Homo sapiens.
XX	XX	US2003040070-A1.
XX	XX	27-FEB-2003.
XX	XX	27-JUN-2002; 2002US-00184627.
XX	XX	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997;	97US-0059266P.
PR	17-OCT-1997;	97US-0062250P.
PR	21-OCT-1997;	97US-0063486P.
PR	24-OCT-1997;	97US-0063120P.
PR	24-OCT-1997;	97US-0063121P.
PR	28-OCT-1997;	97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066468P.
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PR 11-DEC-1997; 97US-0069333P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
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QY	121	ACACACACAAATTTACACAGGACCCCAAGGAGATGATGGTCAAAAAGGAGATCCAGAGAA	180
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QY	181	GAGGAAAGCATGGCAAAAGTGGGACGCAATGGGGCCGAAAGGAATTAAGAGGAATCTGGGT	240
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QY	301	GGGGAAAAAGTTTCGTTGGAAATCTTGGCAAAAGGCAAAAGGACGATCTGTCTGTGAT	360
Db	322	GGGGAAAAAGTTTCGTTGGAAATCTTGGCAAAAGGCAAAAGGACGATCTGTCTGTGAT	381
QY	361	TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCGGCTCAAGACA	420
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QY	61	TTGCAAAATTCAGAGTCTGGGTCGATATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120		
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QY	121	ACACACACAAATTTACACAGAGCCCAAGAGAGATGATGGTGAAAAGAGAGATCCAGAGAA	180		
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DB	262	GATATGGAGATCGGGGCAATATTTGGCAAGCTGGGCGCCATTTGGGAAGAGGGTGACAA	321		
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DB	322	GGGGAAAAAGGTTTGTCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT	381		
QY	361	TGTGGAGATACCGGAATTTGTTGGCAACTGGATATAGTATTCCTCCGCTCAAGACA	420		
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DB	502	TACATCGTCGAGAGACAGAACTACAGAGGAATCCCTAACCCACTGCAGGAATTCGGGGT	561		
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QY	721	GACCCCTATGGTCATGAGCACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	780		
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XX chondrocyte differentiation; tumour necrosis factor-alpha release; ss;
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Best Local Similarity 99.6%; Pred. No. 0;

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 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
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 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy; gene; ss.
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 XX
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 PD 06-FEB-2003.
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XX Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; gene; ss.

OS Homo sapiens.

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PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
PR 17-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096857P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 17:41:22 ; Search time 68 Seconds
(without alignments)

6781.826 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA:*

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- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	2.4	6674	4	US-09-620-312D-110
2	20	2.4	6674	4	US-09-620-312D-110
3	19	2.3	5056	2	US-08-793-136-2
4	19	2.3	5056	3	US-09-132-271-2
5	19	2.3	5067	3	US-09-142-334-23
6	19	2.3	5129	4	US-09-566-921-107
7	18	2.2	1272	4	US-09-252-991A-15539
8	18	2.2	1618	4	US-09-489-847-82
9	18	2.2	20598	4	US-09-593-995-10
10	18	2.2	161652	4	US-09-497-855A-40
11	17	2.0	102	4	US-09-242-890-33
12	17	2.0	477	4	US-09-621-976-132
13	17	2.0	672	4	US-09-242-890-29
14	17	2.0	837	4	US-09-489-039A-686
15	17	2.0	854	4	US-09-401-064-329
16	17	2.0	1497	4	US-09-461-325-48
17	17	2.0	1497	4	US-10-012-542-48
18	17	2.0	1555	4	US-09-227-357-25
19	17	2.0	2214	4	US-08-513-278-3
20	17	2.0	2214	6	US-08-513-278-3
21	17	2.0	2382	4	US-09-641-741-1
22	17	2.0	2719	3	US-08-706-216-1
23	17	2.0	2719	4	US-09-650-284B-1
24	17	2.0	3934	4	US-09-023-655-1066
25	17	2.0	4049	1	US-08-162-809-17
26	17	2.0	4097	1	US-08-162-809-11
27	17	2.0	5406	4	US-08-961-527-166

Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 24, Appli
Sequence 10, Appli
Sequence 3370, Ap
Sequence 48, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-620-312D-110
; Sequence 110, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_fl_genes Version 1.0
; SEQ ID NO 110
; LENGTH: 6674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1312)..(6330)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6674)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-110

Query Match 2-48; Score 20; DB 4; Length 6674;
Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 292 GGTGACAAAGGGGAAAAGG 311
 Db 2188 GGTGACAAAGGGGAAAAGG 2207

RESULT 2
 US-09-620-312D-110/c
 ; Sequence 110, Application US/09620312D
 ; Patent No. 6569662
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhou, Fing
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: John Tillinghaast
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 ; FILE REFERENCE: Polypeptides
 ; CURRENT APPLICATION NUMBER: US/09/620,312D
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 1105
 ; SOFTWARE: Pt_FL_Genes Version 1.0
 ; SEQ ID NO 110
 ; LENGTH: 6674
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1312)..(6330)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(6674)
 ; OTHER INFORMATION: n = a,t,c or g
 US-09-620-312D-110

Query Match 2.4%; Score 20; DB 4; Length 6674;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 GGTGACAAAGGGGAAAAGG 311
 Db 231 GGTGACAAAGGGGAAAAGG 212

RESULT 3
 US-08-793-126-2
 ; Sequence 2, Application US/08793126
 ; Patent No. 5849297
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Richard Alexander
 ; APPLICANT: Faries, Charles Timothy
 ; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HALE AND DORR LLP
 ; STREET: 60 State Street
 ; CITY: Boston

STATE: MA
 COUNTRY: United States of America
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/793,126
 FILING DATE: 07-FEB-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Baker, Hollie L.
 REGISTRATION NUMBER: 31,321
 REFERENCE/DOCKET NUMBER: 102286.377
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 526-6000
 TELEFAX: (617) 526-5000
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5056 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-793-126-2

Query Match 2.3%; Score 19; DB 2; Length 5056;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 AGAGAAATTCCTACTACATC 486
 Db 766 AGAGAAATTCCTACTACATC 784

RESULT 4
 US-09-132-271-2
 ; Sequence 2, Application US/09132271
 ; Patent No. 6221657
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Richard Alexander
 ; APPLICANT: Faries, Charles Timothy
 ; TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HALE AND DORR LLP
 ; STREET: 60 State Street
 ; CITY: Boston
 STATE: MA
 COUNTRY: United States of America
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/132,271
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/793,126
 FILING DATE: 07-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Baker, Hollie L.
 REGISTRATION NUMBER: 31,321
 REFERENCE/DOCKET NUMBER: 102286.377
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 526-6000
 TELEFAX: (617) 526-5000
 INFORMATION FOR SEQ ID NO: 2:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5056 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-132-271-2

Query Match      2.3%; Score 19; DB 3; Length 5056;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 AGAGAAATTTCTACTACATC 486
DB 766 AGAGAAATTTCTACTACATC 784

RESULT 5
US-09-142-334-23
; Sequence 23, Application US/09142334
; Patent No. 6268485
; GENERAL INFORMATION:
; APPLICANT: Farries, Timothy C.
; APPLICANT: Harrison, Richard A.
; TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
; FILE REFERENCE: 4-30443/A/IMU/PCT
; CURRENT APPLICATION NUMBER: US/09/142,334
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: PCT/GB97/00603
; EARLIER FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 5067
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-142-334-23

Query Match      2.3%; Score 19; DB 3; Length 5067;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 AGAGAAATTTCTACTACATC 486
DB 777 AGAGAAATTTCTACTACATC 795

RESULT 6
US-09-566-921-107
; Sequence 107, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-03-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 107
; LENGTH: 5129
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6682888 1000186.8
US-09-566-921-107

Query Match      2.3%; Score 19; DB 4; Length 5129;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 AGAGAAATTTCTACTACATC 486
DB 792 AGAGAAATTTCTACTACATC 810

RESULT 7
US-09-252-991A-15539
; Sequence 15539, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15539
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15539

Query Match      2.2%; Score 18; DB 4; Length 1272;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 GATAGCCGTCCTACCGCT 108
DB 684 GATAGCCGTCCTACCGCT 701

RESULT 8
US-09-489-847-82
; Sequence 82, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 1618
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-82

Query Match      2.2%; Score 18; DB 4; Length 1618;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 GAACGGTGACAAAGCGGA 305
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Db 312 GAAGGTCACAAAGGGGA 329

RESULT 9

US-09-593-995-10

Sequence 10, Application US/09593995

Patent No. 640688

GENERAL INFORMATION:

APPLICANT: Conklin, Darrell C.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA33

FILE REFERENCE: 99-38

CURRENT APPLICATION NUMBER: US/09/593,995

CURRENT FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: 60/139,121

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 10

LENGTH: 20598

TYPE: DNA

ORGANISM: Homo sapiens

US-09-593-995-10

Query Match 2.2%; Score 18; DB 4; Length 20598;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 AAAGGATCCAGGAGAA 180

Db 3000 AAAGGATCCAGGAGAA 3017

RESULT 10

US-09-497-855A-40

Sequence 40, Application US/09497855A

Patent No. 6605432

GENERAL INFORMATION:

APPLICANT: Huang, Tim

TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION

FILE REFERENCE: UMO1523

CURRENT APPLICATION NUMBER: US/09/497,855A

CURRENT FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: 60/120,592

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: 60/118,760

PRIOR FILING DATE: 1999-02-05

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn version 3.0

SEQ ID NO 40

LENGTH: 161652

TYPE: DNA

ORGANISM: Homo sapiens;

US-09-497-855A-40

Query Match 2.2%; Score 18; DB 4; Length 161652;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 GCTGAAGTCTGTGCCACA 123

Db 10158 GCTGAAGTCTGTGCCACA 10175

RESULT 11

US-09-242-890-33

Sequence 33, Application US/09242890

Patent No. 6613887

GENERAL INFORMATION:

APPLICANT: Ogi, Kasuhiro

APPLICANT: Onda, Haruo

TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE

FILE REFERENCE: 2417US0P

; CURRENT APPLICATION NUMBER: US/09/242,890

; CURRENT FILING DATE: 1999-02-28

; PRIOR APPLICATION NUMBER: PCT/JP97/03194

; PRIOR FILING DATE: 1997-08-10

; PRIOR APPLICATION NUMBER: JP 8-240880

; PRIOR FILING DATE: 1996-09-11

; PRIOR APPLICATION NUMBER: JP 8-318049

; PRIOR FILING DATE: 1996-11-28

; PRIOR APPLICATION NUMBER: JP 9-135633

; PRIOR FILING DATE: 1997-05-27

; NUMBER OF SEQ ID NOS: 35

SOFTWARE:

SEQ ID NO 33

LENGTH: 102

TYPE: DNA

ORGANISM: Rat

US-09-242-890-33

Query Match 2.0%; Score 17; DB 4; Length 102;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TCTGGTCTCGATATTG 91

Db 65 TCTGGTCTCGATATTG 81

RESULT 12

US-09-621-976-132

Sequence 132, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 132

LENGTH: 477

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 124..477

NAME/KEY: sig_peptide

LOCATION: 124..273

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 6

OTHER INFORMATION: seq LFTLLSLWMLFP/AE

NAME/KEY: misc_feature

LOCATION: 394

OTHER INFORMATION: n=a, g, c or t

US-09-621-976-132

Query Match 2.0%; Score 17; DB 4; Length 477;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 GAAGAGGAAAGCATGG 194

Db 307 GAAGAGGAAAGCATGG 323

RESULT 13

US-09-242-890-29

Sequence 29, Application US/09242890

Patent No. 6613887

GENERAL INFORMATION:

APPLICANT: Ogi, Kasuhiro

; APPLICANT: Onda, Haruo
; TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
; FILE REFERENCE: 2417USOP
; CURRENT APPLICATION NUMBER: US/09/242,890
; CURRENT FILING DATE: 1999-02-28
; PRIOR APPLICATION NUMBER: PCT/JP97/03194
; PRIOR FILING DATE: 1997-08-10
; PRIOR APPLICATION NUMBER: JP 8-240880
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: JP 8-318049
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: JP 9-135633
; PRIOR FILING DATE: 1997-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE:
; SEQ ID NO 29
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Rat
US-09-242-890-29

Query Match 2.0%; Score 17; DB 4; Length 672;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TCTGGGCTCTGGATATTG 91
|||||
Db 65 TCTGGGCTCTGGATATTG 81

RESULT 14
US-09-489-039A-686/c
; Sequence 686, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 686
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-686

Query Match 2.0%; Score 17; DB 4; Length 837;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 AAGGGTGACAAAGGGGA 305
|||||
Db 102 AAGGGTGACAAAGGGGA 86

RESULT 15
US-09-401-064-329/c
; Sequence 329, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C2
; CURRENT APPLICATION NUMBER: US/09/401,064
; CURRENT FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 329
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(854)
; OTHER INFORMATION: n = A,T,C or G
US-09-401-064-329

Query Match 2.0%; Score 17; DB 4; Length 854;
Best Local Similarity 100.0%; Pred.No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 TGTGATTGTGGAAGATA 371
|||||
Db 573 TGTGATTGTGGAAGATA 557

Search completed: March 11, 2004, 18:52:38
Job time : 71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:44:32 ; Search time 361 Seconds
(without alignments)
8474.814 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831
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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2432557 seqs, 1840798884 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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- 3: /cgm2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgm2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgm2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 17: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	678	81.6	1016	9	US-09-778-597-96
3	678	81.6	1016	9	US-09-778-192A-96
4	678	81.6	1016	9	US-09-778-832A-96
5	678	81.6	1016	10	US-09-778-189-96
6	678	81.6	1016	10	US-09-778-608A-96
7	678	81.6	1016	10	US-09-778-585A-96
8	678	81.6	1016	10	US-09-778-191A-96
9	678	81.6	1016	10	US-09-778-403A-96
10	678	81.6	1016	10	US-09-778-564A-96
11	678	81.6	1016	10	US-09-778-833A-96
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ALIGNMENTS

RESULT 1

US-09-778-295A-96
; Sequence 96 Application US/0978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pooni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630FIC11
; CURRENT APPLICATION NUMBER: US/09/778,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

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2 PRIOR APPLICATION NUMBER: 60/062250
3 PRIOR FILING DATE: 1997-10-17
4 PRIOR APPLICATION NUMBER: 60/064249
5 PRIOR FILING DATE: 1997-11-03
6 PRIOR APPLICATION NUMBER: 60/065311
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Query Match 81.6%; Score 678; DB 9; Length 1016;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 3

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 ; Patent No. US20020177553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
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 ; APPLICANT: Goddard, Audrey
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; APPLICANT: Kljavin, Ivar J.
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 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
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 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C9
 ; CURRENT APPLICATION NUMBER: US/09/978,192A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 81.6%; Score 678; DB 9; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGAATGGCTTTGCATCCTTGGCTTCGAAGAACCAATTTATCTCTCTGTACTATTCTT	60
Db	22	ATGAATGGCTTTGCATCCTTGGCTTCGAAGAACCAATTTATCTCTCTGTACTATTCTT	81
QY	61	TTGCAAAATTCAGAGTCGGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCGGGTCTGGATATTGATAGCGCTCCTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACAAATTTCCAGACCCCAAGAGATGATGGTGAAAGAGAGATCCAGAGAA	180
Db	142	ACACACAAATTTCCAGACCCCAAGAGATGATGGTGAAAGAGAGATCCAGAGAA	201
QY	181	GAGGAAAGCATGCAAAAGTGGGACGATGGGGCCGAAAGGAAATTAAGAGAACTTGGGT	240
Db	202	GAGGAAAGCATGCAAAAGTGGGACGATGGGGCCGAAAGGAAATTAAGAGAACTTGGGT	261
QY	241	GATATGGGAGATCGGGCAATATTGGCAAGACTTGGGCCCATTTGGGGAAGAGGTGACAA	300
Db	262	GATATGGGAGATCAGGGCAATATTGGCAAGACTTGGGCCCATTTGGGGAAGAGGTGACAA	321
QY	301	GGGGAAGAGTGTGGTGGTGAATACCTGGAGAAAGGCAAGCAGGTACTGTCTGTGAT	360
Db	322	GGGGAAGAGTGTGGTGGTGAATACCTGGAGAAAGGCAAGCAGGTACTGTCTGTGAT	381
QY	361	TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTTCCCGGCTCAAGACA	420
Db	382	TGTGGAAGATACCGGAAATTTGTGGCAACTGGATATTAGTATTTCCCGGCTCAAGACA	441
QY	421	TCTATGAAGTTGTCAAGATGTAGCAGGATTTAGGGAAGTCTGAAGAAATTTCTAC	480
Db	442	TCTATGAAGTTGTCAAGATGTAGCAGGATTTAGGGAAGTCTGAAGAAATTTCTAC	501
QY	481	TACATCGTCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	540

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Query Match 81.6%; Score 678; DB 9; Length 1016;
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QY	1	ATGAATGCTTTTGCATCCTTCTCGAAGAACCAATTTATCTCTCTGCTACTATTCTT	60
DB	22	ATGAATGCTTTTGCATCCTTCTCGAAGAACCAATTTATCTCTCTGCTACTATTCTT	81
QY	61	TTGCAATTCAGAGTCTGGCTCTGGATATTGATAGCGCTCTACCCCTGAAGTCTGTGCC	120
DB	82	TTGCAATTCAGAGTCTGGCTCTGGATATTGATAGCGCTCTACCCCTGAAGTCTGTGCC	141
QY	121	ACACACAAATTTCCACAGACCCCAAGGAGATGATGGTGAAGAGGAGATCCAGGAGAA	180
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DB	262	GATATGGAGATCGGGCAATATTGGCAGACTGGGCCCATTTGGGAAGAGGAGGTGACAA	321
QY	301	GGGAAAAAGGTTTGTGGAATACCTGGAGAAAAAGGCAAGACAGGTACTCTGTGTAT	360
DB	322	GGGAAAAAGGTTTGTGGAATACCTGGAGAAAAAGGCAAGACAGGTACTCTGTGTAT	381
QY	361	TGTGAGAGATACCGGAATTTGTGCACTGGATATTAGTATTCCTCCGGCTCAAGACA	420
DB	382	TGTGAGAGATACCGGAATTTGTGCACTGGATATTAGTATTCCTCCGGCTCAAGACA	441
QY	421	TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATAGGGAACCTGAAGAGAAATCTAC	480
DB	442	TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATAGGGAACCTGAAGAGAAATCTAC	501
QY	481	TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	540
DB	502	TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT	561
QY	541	GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTGCC	600
DB	562	GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTGCC	621
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DB	622	AAGAGTGGCTTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGAGGACAGTAC	681
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DB	682	ATGTTTCACAGACAACTCCACTGCAGAACTATAGCACTGGGAATGAGGGGGAACCCAGC	741
QY	721	GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGTCTGTGGCAGATGGAATGACAA	780
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QY	781	GAGTGGCATCTTACCAGTACTTTGTCTGTGAGTTCTATCAAGAGAGAAAAAG	831
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 US-09-978-189-96
 ; Sequence 96, Application US/0978189
 ; Publication No. US20030004102A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acetated and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
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Query Match      81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  ATGAATGGCTTTGTCATCTTGGTTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 60
Db      22  ATGAATGGCTTTGTCATCTTGGTTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 81

Qy      61  TTGCAATTCAGAGTCTGGTCTGGATTTGATAGCCCTCTACCGCTGAAGTCTGTGCC 120
Db      82  TTGCAATTCAGAGTCTGGTCTGGATTTGATAGCCCTCTACCGCTGAAGTCTGTGCC 141

Qy      121  ACACACACAAATTTCCACAGGACCCAAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
Db      142  ACACACACAAATTTCCACAGGACCCAAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 201

Qy      181  GAGGGAAGCATGGCAATGGGACGATGGGCGGAAAGGAATTAAGAGGAATCTGGGT 240
Db      202  GAGGGAAGCATGGCAATGGGACGATGGGCGGAAAGGAATTAAGAGGAATCTGGGT 261

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Qy      241  GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCAGAA 300
Db      262  GATATGGAGATCAGGGCAATATTTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCAGAA 321

Qy      301  GGGGAAAAAGGTTTGGTTCGGAATACCTGGAGAAAAAGGCAAGAGGTACTGTCTGTGAT 360
Db      322  GGGGAAAAAGGTTTGGTTCGGAATACCTGGAGAAAAAGGCAAGAGGTACTGTCTGTGAT 381

Qy      361  TGTGAGATACCGGAAATTTTGTGGCAACTGTGATATTTAGTATTTGCCGGCTCAAGACA 420
Db      382  TGTGAGATACCGGAAATTTTGTGGCAACTGTGATATTTAGTATTTGCCGGCTCAAGACA 441

Qy      421  TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC 480
Db      442  TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCAAGAGAAATTTCTAC 501

Qy      481  TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT 540
Db      502  TACATCGTCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGT 561

Qy      541  GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTGCC 600
Db      562  GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTGCC 621

Qy      601  AAGATGGCTTTCTTTTCGGGTCTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db      622  AAGATGGCTTTCTTTTCGGGTCTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681

Qy      661  ATGTTTCAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC 720
Db      682  ATGTTTCAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCAGC 741

Qy      721  GACCCCTATGCTATGAGGACTGTGTGAGATGCTGAGCTCTGCGAGTGAATGACACA 780
Db      742  GACCCCTATGCTATGAGGACTGTGTGAGATGCTGAGCTCTGCGAGTGAATGACACA 801

Qy      781  GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAGAAAAAG 831
Db      802  GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAGAAAAAG 852

RESULT 6
US-09-978-608A-96
; Sequence 96, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Aekhenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

```

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC22
;; CURRENT APPLICATION NUMBER: US/09/378,608A
;; CURRENT FILING DATE: 2001-10-16
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 96
;; LENGTH: 1016
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-978-608A-96

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
DB 22 ATGAATGGCTTTGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 81

QY 61 TTGCAAAATTCAGAGTCTGGGTCTCGATATTTGATAGCGTCTCCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTCGATATTTGATAGCGTCTCCGCTGAAGTCTGTGCC 141

QY 121 ACACACACAAATTTCCAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAAATTTCCAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGCAAGAAAGAAATTAAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGCAAGAAAGAAATTAAGGAGAACTGGGT 261

QY 241 GATATGGGAGATCGGGCAATATTTGCAAGATCTGGGCCCATTTGGGAAGAGGTGACAA 300
DB 262 GATATGGGAGATCGGGCAATATTTGCAAGATCTGGGCCCATTTGGGAAGAGGTGACAA 321

QY 301 GGGGAAAAAGTTTCTGTTGAATACCTGGAAGAAAGGCAAGAGGTCTGTGTAT 360
DB 322 GGGGAAAAAGTTTCTGTTGAATACCTGGAAGAAAGGCAAGAGGTCTGTGTAT 381

QY 361 TGTGAAGATACCGGAATTTGTTGGCACTGTGATATTTAGTATTCCTGGCTCAAGACA 420
DB 382 TGTGAAGATACCGGAATTTGTTGGCACTGTGATATTTAGTATTCCTGGCTCAAGACA 441

QY 421 TCTATGAATTTGTCAAGATTTGATAGCGGATTTAGGAAATCTGAAGAAATTTCTAC 480
DB 442 TCTATGAATTTGTCAAGATTTGATAGCGGATTTAGGAAATCTGAAGAAATTTCTAC 501

QY 481 TACATCGTCAGGAGAGAGAACTACAGGATCCCTAACCCACTGCAGGATTCGGGT 540
DB 502 TACATCGTCAGGAGAGAGAACTACAGGATCCCTAACCCACTGCAGGATTCGGGT 561

QY 541 GGAATGTAGCCATGCCAAGATGAAGTGCACACACTCATCGCTGACTATGTGTGCC 600
DB 562 GGAATGTAGCCATGCCAAGATGAAGTGCACACACTCATCGCTGACTATGTGTGCC 621

QY 601 AAGAGTGGCTTCTTCGGGTCTCATTTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTCGGGTCTCATTTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 681

QY 661 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
DB 682 ATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741

QY 721 GACCCCTATGTCATAGGAGCTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATAGGAGCTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801

QY 781 GAGTGCCTATCTTACCATGACTTTTGTCTGTGAGTTTCAAGAAAGAAAAAG 831
DB 802 GAGTGCCTATCTTACCATGACTTTTGTCTGTGAGTTTCAAGAAAGAAAAAG 852

RESULT 7
US-09-978-585A-96
;; Sequence 96, Application US/09978585A
;; Publication No. US20030049633A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: KJavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC15
;; CURRENT APPLICATION NUMBER: US/09/978,585A
;; CURRENT FILING DATE: 2001-10-16
;; NUMBER OF SEQ ID NOS: 624
;; Prior Application removed - See File Wrapper or Palm
;; SEQ ID NO 96
;; LENGTH: 1016
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-978-585A-96

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 50
DB 22 ATGAATGGCTTTGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 81

QY 61 TTGCAAAATTCAGAGTCTGGGTCTCGATATTTGATAGCGTCTCCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTCGATATTTGATAGCGTCTCCGCTGAAGTCTGTGCC 141

QY 121 ACACACACAAATTTCCAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAAATTTCCAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGCAAGAAAGAAATTAAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGCGAAAGTGGGACGATGGGCGCAAGAAAGAAATTAAGGAGAACTGGGT 261

QY 241 GATATGGGAGATCGGGCAATATTTGCAAGATCTGGGCCCATTTGGGAAGAGGTGACAAA 300
DB 262 GATATGGGAGATCGGGCAATATTTGCAAGATCTGGGCCCATTTGGGAAGAGGTGACAAA 321

QY 301 GGGGAAAAAGTTTCTGTTGAATACCTGGAAGAAAGGCAAGAGGTCTGTGTAT 360
DB 322 GGGGAAAAAGTTTCTGTTGAATACCTGGAAGAAAGGCAAGAGGTCTGTGTAT 381

QY 361 TGTGGAAGATACCGAAATTTGTTGGCAAACTGGGATATTAGTATTGCCCGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGAAATTTGTTGGCAAACTGGGATATTAGTATTGCCCGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGAACTGTGATAGCAGGGATTAGGAACTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGAACTGTGATAGCAGGGATTAGGAACTGAAGAGAAATTTCTAC 501
 QY 481 TACATGTCGACAGAAAGAAAGAACTACAGGGAATCCCTTAACCCACTGCAGGATTTGGGGT 540
 Db 502 TACATGTCGACAGAAAGAAAGAACTACAGGGAATCCCTTAACCCACTGCAGGATTTGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGATGAAGTGAAGTCCCAACACATCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGATGAAGTGAAGTCCCAACACATCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCCGGTGTTTCAATTCGCGTGATGACCTTTGAAAGGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTCTTTCCGGTGTTTCAATTCGCGTGATGACCTTTGAAAGGGAGGACAGTAC 681
 QY 661 ATGTTTCACAGACAACTCCCACTGACAGAACTATACCACTGGATGAGGGAGGCCAGC 720
 Db 682 ATGTTTCACAGACAACTCCCACTGACAGAACTATACCACTGGATGAGGGAGGCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGACAGATGGAATGACACA 780
 Db 742 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGACAGATGGAATGACACA 801
 QY 781 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAG 831
 Db 802 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAG 852

RESULT 8

US-09-978-191A-96
 ; Sequence 96, Application US/09978191A
 ; Publication No. US20030050239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Faoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC4
 ; CURRENT APPLICATION NUMBER: US/09/978.191A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
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 ; PRIOR APPLICATION NUMBER: 60/079656
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;;
Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAATGGCTTTTGCAATCCTTCTGCTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTTT 60
Db 22 ATGAATGGCTTTTGCAATCCTTCTGCTTCGAAGAAACCAATTTATCTCTCTGGTACTATTCTTT 81
QY 61 TTGCAAAATTTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTTACCCTGTAAGTCTGTGCC 120
Db 82 TTGCAAAATTTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTTACCCTGTAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCAGAGCCCAAGAGGAGATGATGTGAAAAGAGAGATCCAGAGAA 180
Db 142 ACACACAAATTTCCAGAGCCCAAGAGGAGATGATGTGAAAAGAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGCAAGTGGGACGATCGGCGCAAGGAAATTAAGAGAGAACTGGGT 240
Db 202 GAGGAAAGCATGCAAGTGGGACGATCGGCGCAAGGAAATTAAGAGAGAACTGGGT 261
QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 300
Db 262 CATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 321
QY 301 GGGGAAAAGGTTTGTGGAAATACCTGGAGAAAGGCAAGCAGGACTGCTCTGTAT 360
Db 322 GGGGAAAAGGTTTGTGGAAATACCTGGAGAAAGGCAAGCAGGACTGCTCTGTAT 381
QY 361 TGTGAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTTCCCGGCTCAAGACA 420
Db 382 TGTGAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTTCCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAATCTGAAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAATCTGAAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTATCCTGCTGACTATGTGCC 600
Db 562 GGAATGTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTATCCTGCTGACTATGTGCC 621
QY 601 AAGAGTGGCTTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
Db 682 ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATCTGAGCTCTGGCAGATGGAATGACACA 801

Qy 781 GAGTGCCTTACCATGACTTCTGCTGAGTTTCATCAGAGAAAAG 831
Db 802 GAGTGCCTTACCATGACTTCTGCTGAGTTTCATCAGAGAAAAG 852

RESULT 9

US-09-978-403A-96
; Sequence 96 Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: KJjavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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/ PRIOR APPLICATION NUMBER: 60/085697

Query Match      81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  ATGAATGCTTTGATCTCTTCGAGAAACCAATTTATCTCTCTGGTACTATTTCCT 60
DB      22  ATGAATGCTTTGATCTCTTCGAGAAACCAATTTATCTCTCTGGTACTATTTCCT 81
QY      61  TTGCAAAATCAGATCGGTGCTCGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120

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DB      82  TTGCAAAATTCAGACTCTGGGCTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
QY      121 ACACACAAATTTCCACGAGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB      142 ACACACAAATTTCCACGAGACCCAAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201
QY      181 GAGGAAAGCATGCGCAAGTGGGACGCTATGGGCCGAAAGGAAATTAAGAGAACTGGGCT 240
DB      202 GAGGAAAGCATGCGCAAGTGGGACGCTATGGGCCGAAAGGAAATTAAGAGAACTGGGCT 261
QY      241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGAGGTGACAA 300
DB      262 GATATGGAGATCAGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGAGGTGACAA 321
QY      301 GGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGGCAAGCAAGCTACTGTCTGTAT 360
DB      322 GGGGAAAAAGTTTGTCTTGAATACCTGGAGAAAAAGGCAAGCAAGCTACTGTCTGTAT 381
QY      361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGCTGATATTAGTATTTCCCGGCTCAAGACA 420
DB      382 TGTGGAAGATACCGGAAATTTGTTGGCAACTGCTGATATTAGTATTTCCCGGCTCAAGACA 441
QY      421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTTAGGAAACTGAAGAGAAATTTCTAC 480
DB      442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTTAGGAAACTGAAGAGAAATTTCTAC 501
QY      481 TACATCTGCGAGAGAGAACTACAGGGATCCCTAACCCACTGCAGGATTCGGGCT 540
DB      502 TACATCTGCGAGAGAGAACTACAGGGATCCCTAACCCACTGCAGGATTCGGGCT 561
QY      541 GGAATGCTAGCCATGCCCAGGATGAAGCTGCCAAACACACTCATCTGCTGACTATGTTGCC 600
DB      562 GGAATGCTAGCCATGCCCAGGATGAAGCTGCCAAACACACTCATCTGCTGACTATGTTGCC 621
QY      601 AAGATGGCTCTTCTGGGTGTTTCATGCGGTGAATGACCTTGAAGAGGAGGACAGTAC 660
DB      622 AAGATGGCTCTTCTGGGTGTTTCATGCGGTGAATGACCTTGAAGAGGAGGACAGTAC 681
QY      661 ATGTTTACAGACAACACTCCACTGCGAAGACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
DB      682 ATGTTTACAGACAACACTCCACTGCGAAGACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
QY      721 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB      742 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY      781 GAGTGCCATCTTACCATGTTCTGTTGAGTTTCATCAAGAGAGAAAAG 831
DB      802 GAGTGCCATCTTACCATGTTCTGTTGAGTTTCATCAAGAGAGAAAAG 852

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RESULT 10
US-09-978-564A-96
; Sequence 96, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

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APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US/09/978,564A
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 2001-07-30
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34 PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 22 ATGAATGGCTTTGGCATCTCTTCGAGAAACCAATTTATCTCTCGTGTACTTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTCGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTCGATATTGATAGCGTCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCACGAGCCCAAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
DB 142 ACACACACAATTTCCACGAGCCCAAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
QY 181 GAGGGAAGAGATGCGCAAGTGGGCGCATGGGCGCAAGAGATTAAGGAGAACTGGGT 240
DB 202 GAGGGAAGAGATGCGCAAGTGGGCGCATGGGCGCAAGAGATTAAGGAGAACTGGGT 261
QY 241 GATATGGAGATCGGGCAATATTGGCAAGATCGGGCCATTTGGGAAGAGGGTGACAAA 300
DB 262 GATATGGAGATCGGGCAATATTGGCAAGATCGGGCCATTTGGGAAGAGGGTGACAAA 321
QY 301 GGGGAAAAGGTTTGGTGGATACCTGGGAAAAGGCAAGCAGGTACTCTGTGTAT 360
DB 322 GGGGAAAAGGTTTGGTGGATACCTGGGAAAAGGCAAGCAGGTACTCTGTGTGTAT 381
QY 361 TGTGGAAGATCCGGAAATTTGTTGGCAACTGGATATTAGTATTCGCGGTCAAGACA 420
DB 382 TGTGGAAGATCCGGAAATTTGTTGGCAACTGGATATTAGTATTCGCGGTCAAGACA 441
QY 421 TCTATGAATTTGTCAAGATGTGATAGCAGGATAGGGAATCTGAAGAGAAATTTCTAC 480
DB 442 TCTATGAATTTGTCAAGATGTGATAGCAGGATAGGGAATCTGAAGAGAAATTTCTAC 501
QY 481 TACATCGTCGAGGAAGAGAACTACAGGGAATCCCTTAACCCACTGCAGGATTCGGGT 540

DB 502 TACATCGTCGAGGAAGAGAACTACAGGAATCCCTAACCCACTGCAGGATTCGGGT 561
QY 541 GGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTGCC 600
DB 562 GGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTCATCTGCTGACTATGTGCC 621
QY 601 AAGAGTGGCTTCTTTGGGTGTTTCNTTGGCGTGAATGACCTTGAAAGGGGAGACAGTAC 660
DB 622 AAGAGTGGCTTCTTTGGGTGTTTCNTTGGCGTGAATGACCTTGAAAGGGGAGACAGTAC 681
QY 661 ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTATAGCAATGAGGGGAAACCCAGC 720
DB 682 ATGTTCAAGACAACTCCACTGCAGAACTATAGCAACTATAGCAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAG 831
DB 802 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAG 852

RESULT 11
US-09-999-833A-96
; Sequence 96, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632

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PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
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PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGATGGCTTTGCATCCCTTCTTCCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
Db 22 ATGATGGCTTTGCATCCCTTCTTCCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGATATTTAGTATCCCTCTACCGCTGAAGTCTGTGCC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGATATTTAGTATCCCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGGACCCAAAGGAGATGATGTGTAAGAGGAGATCCAGAGAA 180
Db 142 ACACACACAATTTCCAGGACCCAAAGGAGATGATGTGTAAGAGGAGATCCAGAGAA 201
QY 181 GAGGGAACGATCGCAAGTGGGAGCGCATGGGCGCGAAGGAATTAAGAGAACTGGT 240
Db 202 GAGGGAACGATCGCAAGTGGGAGCGCATGGGCGCGAAGGAATTAAGAGAACTGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAA 300
Db 262 GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAA 321
QY 301 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTGAT 360
Db 322 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAATTTCTTGCAACTTGGATATTTAGTATTCCTCCGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAATTTCTTGCAACTTGGATATTTAGTATTCCTCCGCTCAAGACA 441
QY 421 TCTATGAAGTTTCTCAAGATGTGATAGCAGGATAGGGAACCTGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTCTCAAGATGTGATAGCAGGATAGGGAACCTGAAGAGAAATTTCTAC 501
QY 481 TACATGTCGAGAGAGAGAGACTACAGGATCCCTTAACCCACTGCAGGATTCGGGT 540
Db 502 TACATGTCGAGAGAGAGAGACTACAGGATCCCTTAACCCACTGCAGGATTCGGGT 561
QY 541 GGAATCTAGCCATGCCCAAGGATGAAGTGCACACACATCATCGTGTGATTTGCC 600
Db 562 GGAATCTAGCCATGCCCAAGGATGAAGTGCACACACATCATCGTGTGATTTGCC 621
QY 601 AAGAGTGGCTTTCTTCGGGTGTTCTATTCGGTGAATGACCTTGAAGAGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTCTTCGGGTGTTCTATTCGGTGAATGACCTTGAAGAGGAGGACAGTAC 681
QY 661 ATGTTCCACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC 720
Db 682 ATGTTCCACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGTCATGAGAGCTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGAGCTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
QY 781 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAG 831
Db 802 GAGTGCATCTTACCATGTACTTTCTGTGAGTTTCATCAAGAGAAAG 852

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RESULT 12

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; Sequence 96, Application US/09981915A
; Publication No. US2003005496A1
; GENERAL INFORMATION:

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; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630FIC12
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 578; DB 10; Length 1016;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTGCATCCTTGGCTTCGAAAGAAACCAATTTATCTCTCTGGTACTATTTCCT 60
 DB 22 ATGAATGGCTTTTGCATCCTTGGCTTCGAAAGAAACCAATTTATCTCTCTGGTACTATTTCCT 81
 QY 61 TTGCAATTCAGACTCGGCTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
 DB 82 TTGCAATTCAGACTCGGCTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACACAATTTTCCAGAGACCCAAAGAGAGATGATGGTGAATAAGAGATCCAGAGAA 180
 DB 142 ACACACACAATTTTCCAGAGACCCAAAGAGAGATGATGGTGAATAAGAGATCCAGAGAA 201
 QY 181 GAGGAAAGCATGGCAAGTGGGACCGATGGGCGGCAAGCAATTAAGGAGAACTGGGT 240
 DB 202 GAGGAAAGCATGGCAAGTGGGACCGATGGGCGGCAAGCAATTAAGGAGAACTGGGT 261
 QY 241 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATATTGGGAAGAGGCTGACAA 300

Db 262 GATATGGGAGATCAGGCGCAATATGGCGAGACTGGGCCCATTTGGGAAGAGGTGACAAA 321
QY 301 GGGGAAAAGGTTTGGTGGAAATCTGGAATCTGGAAGAAAAGGCAAGGATGCTGTGTGAT 360
Db 322 GGGGAAAAGGTTTGGTGGAAATCTGGAATCTGGAAGAAAAGGCAAGGATGCTGTGTGAT 381
QY 361 TGTGGAAGATACCGGAATTTGTTGGACAACTGGGATATTAGTATTTGCCGCTCAAGACA 420
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QY 421 TCTATGAATTTGTTCAAGAAATGTTAGTACAGGATTTAGGAAAATCTGAAGAAAATTTCTAC 480
Db 442 TCTATGAATTTGTTCAAGAAATGTTAGTACAGGATTTAGGAAAATCTGAAGAAAATTTCTAC 501
QY 481 TACATCGTGCAGAGAGAGAACTTACAGGAAATCCCTTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGAGAGAGAACTTACAGGAAATCCCTTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCATCCCAAGATGAAGCTGCCAACAACACTCATCGCTGACTATGTTGCC 600
Db 562 GGAATGCTAGCATCCCAAGATGAAGCTGCCAACAACACTCATCGCTGACTATGTTGCC 621
QY 601 AAGAGTGCTCTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGCTCTTCTTCGGGTGTTCAATGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
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QY 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCGAGATGGATGACACA 780
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QY 781 GAGTGCCATCTTACCATGATCTTGTCTGTGAGTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCCATCTTACCATGATCTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 13
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; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTGATCCTCTTGCTTGAAGAAACCAATTTATCCTCTGTGACTATTCTT 60
Db 22 ATGAATGGCTTTTGATCCTCTTGCTTGAAGAAACCAATTTATCCTCTGTGACTATTCTT 81
QY 61 TTGCAATTCAGACTCTGGCTCTGGATTTGATAGCGCTTACCGCTGAAGTCTGTGCC 120
Db 82 TTGCAATTCAGACTCTGGCTCTGGATTTGATAGCGCTTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCACGAGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
Db 142 ACACACACAATTTCCACGAGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGCAAAAGTGGGACCGCTGGGCGGCAAGGATTAAGAGAACTGGCT 240
Db 202 GAGGAAAGCATGCAAAAGTGGGACCGCTGGGCGGCAAGGATTAAGAGAACTGGCT 261
QY 241 GATATGGGAGATCGGGCAATTTTGGCAACATTTGGGCGCCATTTGGGAGAGGGTGCACAA 300
Db 262 GATATGGGAGATCAGGGCAATTTTGGCAACATTTGGGCGCCATTTGGGAGAGGGTGCACAA 321
QY 301 GGGGAAAAAGGTTTGGCTTGGATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTAT 360
Db 322 GGGGAAAAAGGTTTGGCTTGGATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTAT 381
QY 361 TGTGGAAGATACCGGAAATTTTGGGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAAATTTTGGGACAACTGGATATTAGTATTGCCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGCAGAAATGTGATAGCGGGATTAAGGAAACTGAAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGCAGAAATGTGATAGCGGGATTAAGGAAACTGAAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGATATGTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGATATGTGCC 621
QY 601 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGGTGATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGGTGATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTTCACAGACAAACACTCCACTCCAGAACTATAGCAATGGGAATGAGGGGGAACCCAGC 720

Query Match 81.6%; Score 678; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
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PRIOR APPLICATION NUMBER: 60/086023

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DB 22 ATGAATGCGCTTTGTCATCCCTTGGCTTCGAGAGAAACCAATTTATCTCTCTGTACTATTTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCCCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCCCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCACGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
DB 142 ACACACAAATTTCCACGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGCGCAAGTGGGACGATGGGGCCCAAGAGAAATTAAGAGAACTGGGT 240
DB 202 GAGGAAAGCATGCGCAAGTGGGACGATGGGGCCCAAGAGAAATTAAGAGAACTGGGT 261
QY 241 CATATGGGAGATCGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGGGTGAAGAA 300
DB 262 CATATGGGAGATCAGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGGGTGAAGAA 321
QY 301 GGGGAAAGGTTTGGCTTGGAAATCTGGAGAAAGAGGCAAGCAGTACTGTCTGTGAT 360
DB 322 GGGGAAAGGTTTGGCTTGGAAATCTGGAGAAAGAGGCAAGCAGTACTGTCTGTGAT 381
QY 361 TGTGAAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCGGCTCAAGACA 420
DB 382 TGTGAAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTGCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAACTCAAGAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAAACTCAAGAGAAATTTCTAC 501
QY 481 TACATCGTCGAGGAGAGAAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
DB 502 TACATCGTCGAGGAGAGAAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561
QY 541 GGAATGCTAGCCATGCCPAGGATGAGCTGCCAACACACTCATCTCATCTGCTGCTATGTTGCC 600
DB 562 GGAATGCTAGCCATGCCPAGGATGAGCTGCCAACACACTCATCTCATCTGCTGCTATGTTGCC 621
QY 601 AAGAGTGGCTTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 681
QY 661 ATGTTTCAGAGAACACTCCACTGCAGAACTATAGCACTGGATGAGGGGAAACCCAGC 720
DB 682 ATGTTTCAGAGAACACTCCACTGCAGAACTATAGCACTGGATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGGCAATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAGAAAG 831
DB 802 GAGTGGCAATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAGAAAG 852

RESULT 15
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; Sequence 96, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavil, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 81.6%; Score 678; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGAATGGCTTTGGCATCTCTTGGCTTCGAAGAAACCAATTTATCTCTCGGTACTATTCTT	60
Db	22	ATGAATGGCTTTGGCATCTCTTGGCTTCGAAGAAACCAATTTATCTCTCGGTACTATTCTT	81
Qy	61	TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	141
Qy	121	ACACACAAATTTCCAGGACCCAAAGAGATGATGGTAAAGAGATCCAGGAGAA	180
Db	142	ACACACAAATTTCCAGGACCCAAAGAGATGATGGTAAAGAGATCCAGGAGAA	201
Qy	181	GAGGGAAGCATGGCAAGTGGGACGATGGGCGGAAGGAATTAAGGAGAACTGGGT	240
Db	202	GAGGGAAGCATGGCAAGTGGGACGATGGGCGGAAGGAATTAAGGAGAACTGGGT	261
Qy	241	GATATCGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA	300
Db	262	GATATCGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA	321
Qy	301	GGGGAAGAGGTTGCTTGGATACCTGGGAAGGAAGCAAGCAGGTACTGTCTGTGAT	360
Db	322	GGGGAAGAGGTTGCTTGGATACCTGGGAAGGAAGCAAGCAGGTACTGTCTGTGAT	381
Qy	361	TGTGGAAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCCGCTCAAGACA	420
Db	382	TGTGGAAGATACCGGAAATTTGTTGACAACTGGATATTAGTATTGCCCGCTCAAGACA	441

Qy	421	TCTATGAAGTTTGTCAAGANTGTGATAGCAGGGATTAGGGAACCTGAAGAGAAATTTCTAC	480
Db	442	TCTATGAAGTTTGTCAAGANTGTGATAGCAGGGATTAGGGAACCTGAAGAGAAATTTCTAC	501
Qy	481	TACATCGTGCAGGAAGAGAAACTACAGGGAATCCCTAACCCACTGCGAGGATTCGGGT	540
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Qy	541	GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACACTCATCGCTGACTATGTTGCC	600
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Qy	601	AAGAGTGGCTTCCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC	660
Db	622	AAGAGTGGCTTCCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC	681
Qy	661	ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGNAATGAGGGGNAACCCAGC	720
Db	682	ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGNAATGAGGGGNAACCCAGC	741
Qy	721	GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	780
Db	742	GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA	801
Qy	781	GAGTGCCATCTTACCATGTACTTTGTGTGAGTTTCATCAAGAGAGAAAAG	831
Db	802	GAGTGCCATCTTACCATGTACTTTGTGTGAGTTTCATCAAGAGAGAAAAG	852

Search completed: March 11, 2004, 20:36:29
 Job time : 365 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:36:34 ; Search time 2526 Seconds
(without alignments)
9824.019 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatgcttgatcctt.....agttcatcaagaagaaag 831

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: gb_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	✓ 87.7	834	29 AY409410	Homo sapi
2	608	73.2	834	29 AY409411	Pan trogl
3	523	62.9	752	12 BM009998	603630745
4	401	48.3	609	12 BM010788	603629302

5	364	43.8	560	13	BM494095
6	356	42.8	457	13	BM496500
7	228	27.4	747	14	CB228545
8	153	18.4	1239	12	BM551435
9	148	17.8	326	14	R29493
10	148	17.8	670	14	CB141360
11	138	16.6	735	13	BM090456
12	116	14.0	362	14	R97480
13	75	9.0	354	10	AM435866
14	75	9.0	492	10	BF078010
15	72	8.7	357	9	AV653117
16	71	8.5	499	12	BI467460
17	48	5.8	368	14	W00944
18	29	3.5	636	13	BM671934
19	29	3.5	783	29	CC909869
20	28	3.4	834	29	AY409412
21	28	3.4	955	10	BM612129
22	28	3.4	4591	11	AK028423
23	26	3.1	324	13	BY331120
24	26	3.1	325	13	BY332718
25	26	3.1	361	10	BB869996
26	26	3.1	701	29	CE765022
27	23	2.8	344	13	BY008444
28	23	2.8	380	10	BB869893
29	23	2.8	613	13	CA052606
30	22	2.6	246	10	BF881627
31	22	2.6	553	14	CA817970
32	22	2.6	703	14	CB467812
33	22	2.6	823	14	CK147387
34	21	2.5	473	12	BM571216
35	21	2.5	486	12	BM426695
36	21	2.5	515	28	AQ972105
37	21	2.5	529	12	BM571381
38	21	2.5	590	9	AV699021
39	21	2.5	654	12	BI067078
40	21	2.5	780	28	BZ198292
41	21	2.5	872	14	CJ755784
42	21	2.5	1000	29	ECA576754
43	20	2.4	121	10	BF020755
44	20	2.4	170	9	AW051664
45	20	2.4	231	10	BB078045

ALIGNMENTS

RESULT 1
AY409410
LOCUS
DEFINITION
Homo sapiens COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY409410
VERSION
AY409410.1
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 834)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 834)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission

SUMMARIES

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source Location/Qualifiers

1..834

gene /organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>834

/gene="COLEC10"

/locus_tag="HCM3548"

ORIGIN

Query Match 87.7%; Score 729; DB 29; Length 834;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 829; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCCTTCTGCTCGAAGAACCAATTTATCTCTCGTACTATTCTT 60

DB 1 ATGAATGGCTTTGCATCCCTTCTGCTCGAAGAACCAATTTATCTCTCGTACTATTCTT 60

QY 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCC 120

DB 61 TTGCAAAATTCAGAGTCTGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCC 120

QY 121 ACACACACAAATTCACAGACCCCAAGAGATGATGCTGAAGAGAGATCCAGAGAA 180

DB 121 ACACACACAAATTCACAGACCCCAAGAGATGATGCTGAAGAGAGATCCAGAGAA 180

QY 181 GAGGAAAGCATGGCAAGTGGGACGATGGGCGGCGAAGGAATTAAGAGAGAACTGGT 240

DB 181 GAGGAAAGCATGGCAAGTGGGACGATGGGCGGCGAAGGAATTAAGAGAGAACTGGT 240

QY 241 GATATGGAGATCGGGCAATTTGGCAAGTGGGCGGCGAAGGAATTAAGAGAGAACTGGT 300

DB 241 GATATGGAGATCGGGCAATTTGGCAAGTGGGCGGCGAAGGAATTAAGAGAGAACTGGT 300

QY 301 GGGGAAAAAGGTTTGTCTGGAATACCTGGAGAAAGCAAGCAGGTACTGTCTGTGAT 360

DB 301 GGGGAAAAAGGTTTGTCTGGAATACCTGGAGAAAGCAAGCAGGTACTGTCTGTGAT 360

QY 361 TGTGGAAGATACCGGAAATTTGTGGCACTGAGTATAGTATGTCCTCGGCTCAAGACA 420

DB 361 TGTGGAAGATACCGGAAATTTGTGGCACTGAGTATAGTATGTCCTCGGCTCAAGACA 420

QY 421 TCTATCAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAAAGCAAGCAAAATTTCTAC 480

DB 421 TCTATCAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAAAGCAAGCAAAATTTCTAC 480

QY 481 TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTTAACCCACTGCGAGATTCGGGGT 540

DB 481 TACATCGTGCAGAGAGAGAACTACAGGAAATCCCTTAACCCACTGCGAGATTCGGGGT 540

QY 541 GGAATCTAGCATGCCCCAAGGATGAGTGCACACACATCATCGCTGACTATGTTGCC 600

DB 541 GGAATCTAGCATGCCCCAAGGATGAGTGCACACACATCATCGCTGACTATGTTGCC 600

QY 601 AAGAGTGGCTCTTTTCGGGTGTTCAATTCGCGTGAATACCTTGAAGAGGGGACAGTAC 660

DB 601 AAGAGTGGCTCTTTTCGGGTGTTCAATTCGCGTGAATACCTTGAAGAGGGGACAGTAC 660

QY 661 ATGTTTACAGACAACTCCATCGAGAACTATAGCAATCGAATGAGGGGAAACCCAGC 720

DB 661 ATGTTTACAGACAACTCCATCGAGAACTATAGCAATCGAATGAGGGGAAACCCAGC 720

QY 721 GACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780

DB 721 GACCCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780

QY 781 GAGTGCATCTACCATGATCTTGTCTGTGATTCATCAGAGAGAAAG 831

DB 781 GAGTGCATCTACCATGATCTTGTCTGTGATTCATCAGAGAGAAAG 831

RESULT 2

LOCUS AY409411

DEFINITION Pan troglodytes COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY409411

VERSION AY409411.1 GI:39765379

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 834)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 834)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

1..834

source /organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..>834

gene /gene="COLEC10"

/locus_tag="HCM3548"

ORIGIN

Query Match 73.2%; Score 608; DB 29; Length 834;

Best Local Similarity 99.5%; Pred. No. 2;le-288;

Matches 808; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 TGCTTCGAAGAAACCAATTTATCTCTCTGCTGCTATTTCTTTTGCATAATTCAGAGTCTG 79

DB 20 TGCTTCGAAGAAACCAATTTATCTCTCTGCTGCTATTTCTTTTGCATAATTCAGAGTCTG 79

QY 80 GTCGTGATTTGATAGCGCTTACCGCTGAAGTCTGTGCCACACACACATTTCCACGAG 139

DB 80 GTCGTGATTTGATAGCGCTTACCGCTGAAGTCTGTGCCACACACACATTTCCACGAG 139

QY 140 GACCCAAAGGAGATGATGCTGAAGAAAGAGATCCAGAGAGAGGAGGAGCATGGCAAG 199

DB 140 GACCCAAAGGAGATGATGCTGAAGAAAGAGATCCAGAGAGAGGAGGAGCATGGCAAG 199

QY 200 TGGGACCGCATCGGGCCGCAAGAAATTAAGAGAACTCTGGGTGATATGGGAGATCGGGGCA 259

DB 200 TGGGACCGCATCGGGCCGCAAGAAATTAAGAGAACTCTGGGTGATATGGGAGATCGGGGCA 259

QY 260 ATATTGGCAAGACTGGGCCCATTTGGGAAGAGGCTGCAAGGGGAAAAAGGTTTCTTG 319

DB 260 ATATTGGCAAGACTGGGCCCATTTGGGAAGAGGCTGCAAGGGGAAAAAGGTTTCTTG 319

QY 320 GAATACCTTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGATTTGTGAAAGATACCGGAAAT 379

DB 320 GAATACCTTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGATTTGTGAAAGATACCGGAAAT 379

QY 380 TTGTTGGCAACTGGATATTAGTATTGCCCGGCTCAAGCATCTATGAAGTTTGTCAAGA 439

Db 380 TTGTTGGACAACTGGATATAGTATGCTCGCTCAAGACATCTATGAAGTTTCTCAAGA 439
Qy 440 ATGTGATAGCAGGATAGGAAATGAAGAAATCTACTACATCGTGCAGGAAGAGA 499
Db 440 ATGTGATAGCAGGATAGGAAATCTAGGAATCTAGGAATCTACTACATCGTGCAGGAAGAGA 499
Qy 500 AGAATCTACAGGAATCCCTTACCCACTCAGGATTCGGGTGGATCTAGCCATGCCCA 559
Db 500 AGAATCTACAGGAATCCCTTACCCACTCAGGATTCGGGTGGATCTAGCCATGCCCA 559
Qy 560 AGGATGAAGTCCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGTCTTCTTCGGG 619
Db 560 AGGATGAAGTCCCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGTCTTCTTCGGG 619
Qy 620 TGTTCATTGGCTGAATGACCTTGAAGAGGAGGACAGTACATCTTACAGACACACTC 679
Db 620 TGTTCATTGGCTGAATGACCTTGAAGAGGAGGACAGTACATCTTACAGACACACTC 679
Qy 680 CACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCAGCCCTATGTCATGAGG 739
Db 680 CACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCAGCCCTATGTCATGAGG 739
Qy 740 ACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACAGAGTGCCATCTTACCATGT 799
Db 740 ACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACAGAGTGCCATCTTACCATGT 799
Qy 800 ACTTGTCTGTGAGTTCATCAAGAGAAAGAAAG 831
Db 800 ACTTGTCTGTGAGTTCATCAAGAGAAAGAAAG 831

RESULT 3
BM009998
LOCUS 603630745F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:544459 5',
DEFINITION mRNA sequence.
ACCESSION BM009998
VERSION BM009998.1 GI:16524352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCW1923 row: j column: 12
High quality sequence stop: 752.
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:544459"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 62.9%; Score 523; DB 12; Length 752;
Best Local Similarity 99.7%; Pred. No. 1.7e-246;
Matches 623; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 149 GAGATGATGTTGAAAAAGGAGATCCAGGAGAAAGGAAAGCATGGCAAGTGGGACGCA 208
Db 6 GAGATGATGTTGAAAAAGGAGATCCAGGAGAAAGGAAAGCATGGCAAGTGGGACGCA 65
Qy 209 TGGGCGCCGAAAGGAATTAAGGAGAACTGGTGATATGGGAGATCGGGCAATATTGGCA 268
Db 66 TGGGCGCCGAAAGGAATTAAGGAGAACTGGTGATATGGGAGATCAGGCAATATTGGCA 125
Qy 269 AGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAGGTTTCTTGGAAATACCTG 328
Db 126 AGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAGGTTTCTTGGAAATACCTG 185
Qy 329 GAGAAAGGCGAAAGCAGTACTCTGTGATTTGTGGAGATACCGGAATTTTGTGGAC 388
Db 186 GAGAAAGGCGAAAGCAGTACTCTGTGATTTGTGGAGATACCGGAATTTTGTGGAC 245
Qy 389 AACTGGATATTAGTATTTGCCCGGCTCAAGACATCTATGAAGTTTGTCAAGATGTGATAG 448
Db 246 AACTGGATATTAGTATTTGCCCGGCTCAAGACATCTATGAAGTTTGTCAAGATGTGATAG 305
Qy 449 CAGGATTTAGGAACTGAAGAGAAATTTACTACATCTGTCAGGAGAGAGAACTACA 508
Db 306 CAGGATTTAGGAACTGAAGAGAAATTTACTACATCTGTCAGGAGAGAGAACTACA 365
Qy 509 GGGAAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTTAGCCATGCCCAAGGATGAAG 568
Db 366 GGGAAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTTAGCCATGCCCAAGGATGAAG 425
Qy 569 CTGCCAACAACACTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTCGGGTGTTCAATTG 628
Db 426 CTGCCAACAACACTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTCGGGTGTTCAATTG 485
Qy 629 CGGTGAATGACTTTGAAGGGAGGAGCAGTACATGTTTCCAGACACACTCCCACTGCAGA 688
Db 486 CGGTGAATGACTTTGAAGGGAGGAGCAGTACATGTTTCCAGACACACTCCCACTGCAGA 545
Qy 689 ACTATAGCAACTGGATGAGGGGGAACCCAGCAGCCCTATGTCATGAGGACTGTGTGG 748
Db 546 ACTATAGCAACTGGATGAGGGGGAACCCAGCAGCCCTATGTCATGAGGACTGTGTGG 605
Qy 749 AGATGCTGAGCTCTGGCAGATGGAA 773
Db 606 AGATGCTGAGCTCTGGCAGATGGAA 630

BM010788 609 bp mRNA linear EST 30-OCT-2001
LOCUS 603629302F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5434680 5',
DEFINITION mRNA sequence.
ACCESSION BM010788
VERSION BM010788.1 GI:16525142
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 609)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM912 row: c column: 01
High quality sequence stop: 608.
Location/Qualifiers

FEATURES

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1. 609
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/clone="IMAGE:5434680"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 401; DB 12; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.4e-186; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 431 TTGTCAGGAATGTGATGAGCAGGATTTAGGAACTGAGAGAAATTTCTACTACATCGTGC 490
DB 69 TTGTCAGGAATGTGATGAGCAGGATTTAGGAACTGAGAGAAATTTCTACTACATCGTGC 128
QY 491 AGAAGAAGAACTACAGGGAATCCCTAACCCACTGACAGGATTCGGGTGGGAATGCTAG 550
DB 129 AGAAGAAGAACTACAGGGAATCCCTAACCCACTGACAGGATTCGGGTGGGAATGCTAG 188
QY 551 CCATGCCCAAGATGAAGTGTGCTCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCT 610
DB 189 CCATGCCCAAGATGAAGTGTGCTCAACACACTCATCGCTGACTATGTTGCCAAGAGTGGCT 248
QY 611 TCCTTCGGGTGTTCATGTCGGTGAATGACCTTGAAGGGAGGACAGTACATGTTTCAG 670
DB 249 TCCTTCGGGTGTTCATGTCGGTGAATGACCTTGAAGGGAGGACAGTACATGTTTCAG 308
QY 671 ACAACACTCCACTGCAGAACTATAGCACTGAATGAGGGGAAACCCAGACCCCTATG 730
DB 309 ACAACACTCCACTGCAGAACTATAGCACTGAATGAGGGGAAACCCAGACCCCTATG 368
QY 731 GTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATC 790
DB 369 GTCATGAGAACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATC 428
QY 791 TTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAG 831
DB 429 TTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAG 469

RESULT 5

LOCUS BX494095 560 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp779A1511 r1 779 (synonym: hnccl) Homo sapiens cDNA clone
BX494095 DKFZp779A1511 5', mRNA sequence.

ACCESSION

VERSION BX494095 1 GI:32007261

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 560)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,

TITLE

JOURNAL

COMMENT

Fobo,G., Han,M. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DKFZp779A1511) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1. 560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp779A1511"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site 1: SfiI; Site 2: SfiIb"

ORIGIN

Query Match 43.8%; Score 364; DB 13; Length 560;
Best Local Similarity 99.6%; Pred. No. 4.2e-168; Indels 0; Gaps 0;
Matches 464; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGATGCTTTGATCCTCTGCTTCGAAGAAACCAATTTATCTCTCTGTTACTTTCTT 60
DB 95 ATGATGCTTTGATCCTCTGCTTCGAAGAAACCAATTTATCTCTCTGTTACTTTCTT 154
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTACCGCTGAGTCTGTGC 120
DB 155 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTTACCGCTGAGTCTGTGC 214
QY 121 ACACACACAAATTCACAGGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
DB 215 ACACACACAAATTCACAGGACCCAAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 274
QY 181 GAGGAAAGCATGCGAAAGTGGGACCGATGGGCGCGAAGAGATTAAGAGAGACTGGGT 240
DB 275 GAGGAAAGCATGCGAAAGTGGGACCGATGGGCGCGAAGAGATTAAGAGAGACTGGGT 334
QY 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGAACAA 300
DB 335 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGAACAA 394
QY 301 GGGGAAAAAGTTTGTCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 395 GGGGAAAAAGTTTGTCTTGGAAATACCTGGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 454
QY 361 TGTGAGAGATACCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 420
DB 455 TGTGAGAGATACCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGCTCAAGACA 514
QY 421 TCTATGAAGTTTGTCAAGAAATGTCAGCGGATAGGGAACCTG 466
DB 515 TCTATGAAGTTTGTCAAGAAATGTCAGCGGATAGGGAACCTG 560

RESULT 6

LOCUS BX496500

DEFINITION

DKFZp779M0527 r1 779 (synonym: hnccl) Homo sapiens cDNA clone

BX496500 DKFZp779M0527 5', mRNA sequence.

ACCESSION

VERSION BX496500 1 GI:32012178

KEYWORDS

EST 04-SEP-2003
457 bp mRNA linear
Homo sapiens cDNA clone
EST

SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseldorf/Germany) within the cDNA sequencing
consortium of the German genome project. No sl sequence available.
This clone (DKFZ79M0527) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 457
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ79M0527"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="DH10B"
/clone_lib="779 (synonym: hnccl)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"
ORIGIN
Query Match 42.8%; Score 356; DB 13; Length 457;
Best Local Similarity 99.8%; Pred. No. 3.6e-164;
Matches 406; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATGCTTGCATCTCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
DB 27 ATGAATGCTTTCATCTCTTCGAGAAACCAATTTATCTCTCTGCTACTATTTCTT 86
QY 61 TTGCAAAATTCAGATCTGGGTCTGGATATGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
DB 87 TTGCAAAATTCAGATCTGGGTCTGGATATGATAGCGCTCTACCGCTGAAGTCTGTGCC 146
QY 121 ACACACAAATTTACAGGACCCCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 180
DB 147 ACACACAAATTTACAGGACCCCAAGAGAGATGATGGTGAAGAAAGAGATCCAGAGAA 206
QY 181 GAGGAAAGCATGCGCAAGTGGGACGATGGGCGGCAAGAGATTTAAAGGAGAACTGGGT 240
DB 207 GAGGAAAGCATGCGCAAGTGGGACGATGGGCGGCAAGAGATTTAAAGGAGAACTGGGT 266
QY 241 GATATGGAGATCGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGAGGTGACAAA 300
DB 267 GATATGGAGATCGGGCAATATTGGCAAGCTGGGCCCATTTGGGAAGAGAGGTGACAAA 326
QY 301 GGGGAAAAGCTTTGCTTGGATACCTCGAGAAAGGCAAGCAGATCTCTGTGAT 360
DB 327 GGGGAAAAGCTTTGCTTGGATACCTCGAGAAAGGCAAGCAGATCTCTGTGAT 386
QY 361 TGTGGAAGATACCGGAATTTGTTGGCAACTGTGATATTAGTATTCG 407
DB 387 TGTGGAAGATACCGGAATTTGTTGGCAACTGTGATATTAGTATTCG 433
RESULT 7
CB228545
LOCUS
DEFINITION AGNCOURT 11505973 NICHD Rh_Ov1 Macaca mulatta cDNA clone
IMAGE:6886251 5', mRNA sequence.
ACCESSION CB228545

CB228545.1 GI:28280123
EST.
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
1 (bases 1 to 747)
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM3139 row: a column: 02
High quality sequence stop: 526.
Location/Qualifiers
1. 747
/organism="Macaca mulatta"
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/clone="IMAGE:6886251"
/tissue_type="Ovary"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD Rh_Ov1"
/note="Organ: ovary; Vector: pDNR-LIB; Site_1: Sfi I;
Site_2: Sfi I; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.0-4.0 kb. Tissue pooled from
pre-pubertal, post pubertal and menopausal monkeys.
Constructed by Clontech. Note: this is a NICHD Library."
ORIGIN
Query Match 27.4%; Score 228; DB 14; Length 747;
Best Local Similarity 99.4%; Pred. No. 5e-101;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 436 AAGAATGTGATACAGGAACTAGGAACTAGAGAAATTTACTATGTCGTCAGAA 495
DB 3 AAGAATGTGATACAGGAACTAGGAACTAGAGAAATTTACTATGTCGTCAGAA 62
QY 496 GAGAAGAACTACAGGAACTCCCTAACCCACTGAGGATTCGGGGTGAATGCTACCATG 555
DB 63 GAGAAGAACTACAGGAACTCCCTAACCCACTGAGGATTCGGGGTGAATGCTACCATG 122
QY 556 CCCAAGATGAAGCTGCCACACACTGCTGACTATGTTGCCAAGAGTGGCTTTCTTT 615
DB 123 CCCAAGATGAAGCTGCCACACACTGCTGACTATGTTGCCAAGAGTGGCTTTCTTT 182
QY 616 CGGTGTTTCATTGGCTGTAATGACCTTTGAAGGGGAGGACAGTACATGTTTCACAGCAAC 675
DB 183 CGGTGTTTCATTGGCTGTAATGACCTTTGAAGGGGAGGACAGTACGTTTCACAGCAAC 242
QY 676 ACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCAT 735
DB 243 ACTCCACTGAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCAT 302
QY 736 GAGGACTGTGTGAGATGCTGAGCTCTGGC 765
DB 303 GAGGACTGTGTGAGATGCTGAGCTCTGGC 332
RESULT 8
CB228545
LOCUS
DEFINITION AGNCOURT 6579990 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469941
5', mRNA sequence.

```

ACCESSION   BM551435
VERSION     BM551435.1
KEYWORDS    GI:18788489
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1239)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: DCTD/DTF
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLOW1975 row: p column: 06
            High quality sequence start: 38
            High quality sequence stop: 301.
            Location/Qualifiers
                1..1239
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5469941"
                /tissue_type="amelanotic melanoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_41"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; CDNA made by oligo-dT priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            GGCACGAG(G). Library constructed by Ling Hong in the
            laboratory of Gerald M. Rubin (University of California,
            Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
            Superscript II RT (Life Technologies). Note: this is a
            NIH_MGC Library."
            ORIGIN
                Query Match      18.4%; Score 153; DB 12; Length 1239;
                Best Local Similarity 100.0%; Pred. No. 5.1e-64;
                Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAGGTTT 314
Db 137 GGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAGGTTT 196
QY 315 GCTTGGATACCTGGAGAAAGCAAGCAGGCTACTGCTGTGATTGTGGAGATACCG 374
Db 197 GCTTGGATACCTGGAGAAAGCAAGCAGGCTACTGCTGTGATTGTGGAGATACCG 256
QY 375 GAAATTGTTGGCAACTGGATATTAGTATTCG 407
Db 257 GAAATTGTTGGCAACTGGATATTAGTATTCG 289

RESULT 9
R29493
LOCUS      R29493
DEFINITION F1-1006D 22 week old human fetal liver cdna library Homo sapiens
            CDNA clone F1-1006D 5', mRNA sequence.
ACCESSION  R29493
VERSION     R29493.1
KEYWORDS    GI:1511901
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 326)
AUTHORS    Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.

TITLE      Construction of a gene expression profile of a human fetal liver by
            single-pass cDNA sequencing
JOURNAL    Mamm. Genome 6 (9), 653-657 (1995)
MEDLINE    96081342
PUBMED     8535075
COMMENT     Contact: Hee-Sup Shin
            Developmental Genetics
            Pohang Institute of Science & Technology
            San31, Hyodadong Pohang, 790-784 Republic of Korea
            Tel: 562-279-2291
            Fax: 562-279-2199
            Email: shinh@vision.postech.ac.kr
            Seq primer: T3 primer.
            Location/Qualifiers
                1..326
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="F1-1006D"
                /lab_host="X11-blue MRF"
                /clone_lib="22 week old human fetal liver cDNA library"
                /note="Vector: pBluescriptII SK(-); Site 1: EcoRI; Site 2:
            XhoI; The cDNA library made by oligo-dT primed and
            directionally cloned between 5' Exor I-XhoI3' sites."
            ORIGIN
                Query Match      17.8%; Score 148; DB 14; Length 326;
                Best Local Similarity 100.0%; Pred. No. 1.2e-61;
                Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 628
Db 1 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 60
QY 629 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 688
Db 61 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 120
QY 689 ACTATAGCAACTGGAATGAGGGGGAACC 716
Db 121 ACTATAGCAACTGGAATGAGGGGGAACC 148

RESULT 10
LOCUS      CB141360
DEFINITION K-EST0194967 L15CKK1 Homo sapiens cdna clone L15CKK1-30-B10 5',
            mRNA sequence.
ACCESSION  CB141360
VERSION     CB141360.1
KEYWORDS    GI:28116397
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 670)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            Location/Qualifiers
                1..670
                /organism="Homo sapiens"
            ORIGIN
                Query Match      17.8%; Score 148; DB 14; Length 326;
                Best Local Similarity 100.0%; Pred. No. 1.2e-61;
                Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 628
Db 1 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 60
QY 629 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 688
Db 61 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 120
QY 689 ACTATAGCAACTGGAATGAGGGGGAACC 716
Db 121 ACTATAGCAACTGGAATGAGGGGGAACC 148

RESULT 10
LOCUS      CB141360
DEFINITION K-EST0194967 L15CKK1 Homo sapiens cdna clone L15CKK1-30-B10 5',
            mRNA sequence.
ACCESSION  CB141360
VERSION     CB141360.1
KEYWORDS    GI:28116397
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 670)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            Location/Qualifiers
                1..670
                /organism="Homo sapiens"
            ORIGIN
                Query Match      17.8%; Score 148; DB 14; Length 326;
                Best Local Similarity 100.0%; Pred. No. 1.2e-61;
                Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 569 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 628
Db 1 CTGCCACACACTCATCGCTGACTACTATGTTGCCAGAGTGCGTCTCTTGGGGTTCATTG 60
QY 629 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 688
Db 61 GCGTGAATGACCTTGAAGGGGAGGACAGTACATGTTACACACACACTCCACTGCAGA 120
QY 689 ACTATAGCAACTGGAATGAGGGGGAACC 716
Db 121 ACTATAGCAACTGGAATGAGGGGGAACC 148

RESULT 9
R29493
LOCUS      R29493
DEFINITION F1-1006D 22 week old human fetal liver cdna library Homo sapiens
            CDNA clone F1-1006D 5', mRNA sequence.
ACCESSION  R29493
VERSION     R29493.1
KEYWORDS    GI:1511901
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 326)
AUTHORS    Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L15CKK1-30-B10"
/sex="M"
/cell_line="CK-K1"
/lab_host="Top10P"
/clone_lib="L15CKK1"

/note="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP), and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 17.8%; Score 148; DB 14; Length 670;
Best Local Similarity 99.5%; Pred. No. 1.4e-61;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 GAGATGATGGTGAAGAGGATCCAGAGAGAGGAGGAGGATGGCAAGTGGGACGCA 208
DB 236 GAGATGATGGTGAAGAGGATCCAGAGAGAGGAGGAGGATGGCAAGTGGGACGCA 295
QY 209 TGGGCGGAAAGGATTAAGAGGAACTGGGTGATATGGGAGATCGGGGCAATATTGGCA 268
DB 296 TGGGCGGAAAGGATTAAGAGGAACTGGGTGATATGGGAGATCGGGGCAATATTGGCA 355
QY 269 AGACTGGGCGCATTTGGGAGAGGATGACAAAGGGGAAAGGTTTCTTGGGAATACCTG 328
DB 356 AGACTGGGCGCATTTGGGAGAGGATGACAAAGGGGAAAGGTTTCTTGGGAATACCTG 415
QY 329 GAGAAAGGCGCAAGCAGG 347
DB 416 GAGAAAGGCGCAAGCAGG 434

RESULT 11
BX090456
LOCUS
DEFINITION
BX090456 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:1998F03662 ; IMAGE:296450, mRNA sequence.
ACCESSION
BX090456
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 735)
AUTHORS
Ebert, L., Heil, O., Hennig, S., Neubert, P., Patsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
CONTACT: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGE998F03662
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNO=972
CONTACT: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.

FEATURES

source
1..735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998F03662 ; IMAGE:296450"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and spleen; Vector: p7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAAGATTAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 16.6%; Score 138; DB 13; Length 735;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 594 AGCACTGGGATGAGGGGAGCCAGCGACCCCTATGCTCATGAGGACTGTGTGGAGATG 753
DB 1 AGCACTGGGATGAGGGGAGCCAGCGACCCCTATGCTCATGAGGACTGTGTGGAGATG 60
QY 754 CTGAGCTCTGCGAGATGGATGACACAGAGTGCATCTTACCATGTACTTTCTGTGTGAG 813
DB 61 CTGAGCTCTGCGAGATGGATGACACAGAGTGCATCTTACCATGTACTTTCTGTGTGAG 120
QY 814 TTCTATCAAGAGAAAAG 831
DB 121 TTCTATCAAGAGAAAAG 138

RESULT 12
BX090456
LOCUS
DEFINITION
BX090456 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:1998F03662 ; IMAGE:296450, mRNA sequence.
ACCESSION
BX090456
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 362)
AUTHORS
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 1136
High quality sequence stops: 337

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1136 Std Error: 0.00
Seq primer: M13R21
High quality sequence stop: 337.
Location/Qualifiers
1. .362
/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="IMAGE:199539"
/sex="male"
/dev stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: liver and spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES

source

ORIGIN

Query Match 14.0%; Score 116; DB 14; Length 362;
Best Local Similarity 100.0%; Pred. No. 7.5e-46;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 716 CAGGACCCCTATGTCATGAGGACTGTGTGGAGATCTGAGCTCTGGCAGATGGAATG 775
DB 97 CCAGGACCCCTATGTCATGAGGACTGTGTGGAGATCTGAGCTCTGGCAGATGGAATG 156
QY 776 ACACAGAGTGCATCTTACCATGACTTTGTCTGTGAGTTCATCAAGAGAAAAG 831
DB 157 ACACAGAGTGCATCTTACCATGACTTTGTCTGTGAGTTCATCAAGAGAAAAG 212

RESULT 13
AW435866
LOCUS 75149 MARC 2P1G Sus scrofa CDNA 5', mRNA linear EST 09-JUL-2000
DEFINITION 75149 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence.
ACCESSION AW435866
VERSION AW435866.1 GI:6971244
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 354)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keefe,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
JOURNAL 22213789
MEDLINE 12226715
PUBMED

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG

Plate: 30 row: K column: 4
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. .354
/organism="Sus scrofa"
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/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES

source

ORIGIN

Query Match 9.0%; Score 75; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.2e-25;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 CGTCTACCGCTGAAGTCTGTGCCACACACACATTTCCAGGACCCCAAGGAGATGAT 156
DB 123 CGTCTACCGCTGAAGTCTGTGCCACACACACATTTCCAGGACCCCAAGGAGATGAT 182
QY 157 GGTGAAAAGGAGAT 171
DB 183 GGTGAAAAGGAGAT 197

RESULT 14
BF078010
LOCUS 228226 MARC 2P1G Sus scrofa CDNA 5', mRNA linear EST 18-OCT-2000
DEFINITION 228226 MARC 2P1G Sus scrofa CDNA 5', mRNA sequence.
ACCESSION BF078010
VERSION BF078010.1 GI:10871840
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 492)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keefe,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
JOURNAL 22213789
MEDLINE 12226715
PUBMED

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 49 row: P column: 11
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES

source

ORIGIN

Query Match 9.0%; Score 75; DB 10; Length 492;
Best Local Similarity 100.0%; Pred.No.1.3e-25;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 CGTCCTACCGCTGAGTGTGTGCCACACACACAAATTTCCACGAGCCCAAGGAGATGAT 156
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Db 103 CGTCCTACCGCTGAGTGTGTGCCACACACACAAATTTCCACGAGCCCAAGGAGATGAT 162
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QY 157 GGTGAAAAGGAGAT 171
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Db 163 GGTGAAAAGGAGAT 177
|||||

RESULT 15

AV653117 357 bp mRNA linear EST 15-JAN-2002
LOCUS AV653117 GLC Homo sapiens cDNA clone GICDHE09 3', mRNA sequence.
DEFINITION AV653117
ACCESSION AV653117
VERSION AV653117.1 GI:9874131
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 357)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
PUBMED 11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..357
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICDHE09"
/tissue_type="corresponding non cancerous liver tissue"
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/clone_lib="GLC"
/note="Vector: pbluescript sk(-); Site 1: EcoRI; Site 2:
XhoI"

ORIGIN

Query Match 8.7%; Score 72; DB 9; Length 357;
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Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 820 AAGAAGAAAAG 831
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Db 61 AAGAAGAAAAG 72
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 11, 2004, 16:49:43 ; Search time 3293 Seconds
(without alignments)
10937.765 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	831	100.0	1594	9	AB002631 Homo sapi
2	831	100.0	1595	6	E29008 Novel colle
3	826.2	99.4	1016	6	AX376032 Sequence
4	826.2	99.4	1016	9	AY359038 Homo sapi
5	642.8	77.4	867	10	AB016429 Mus muscu
6	390	46.9	141262	9	AC080033 Homo sapi
7	390	46.9	182475	2	AC023487 Homo sapi
8	321.8	38.7	234922	2	AC097055 Rattus no
9	313.8	37.8	168900	2	AC115924 Mus muscu
10	313.8	37.8	22510	2	AC123656 Mus muscu
11	313.8	37.8	345420	2	AC131337 Mus muscu
12	265.4	31.9	1272	5	BC056052 Xenopus l
13	244.6	29.4	813	6	BD103332 Novel col
14	244.6	29.4	1238	6	AR252616 Sequence
15	244.6	29.4	1238	6	AX403469 Sequence
16	244.6	29.4	1238	6	AX454582 Sequence
17	244.6	29.4	1238	6	AX491060 Sequence
18	244.6	29.4	1238	9	AY358439 Homo sapi
19	244.6	29.4	1248	9	BC000078 Homo sapi
20	244.6	29.4	1341	6	BD103302 Novel col
21	239	28.8	813	6	BD103338 Novel col
22	239	28.8	1522	6	BD103307 Novel col
23	233.8	28.1	735	6	BD103333 Novel col
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25	209.8	25.2	741	6	BD103340 Novel col
26	209.8	25.2	1269	6	BD103330 Novel col
27	209.6	25.2	1417	9	BC009951 Homo sapi
28	206.8	24.9	663	6	BD103336 Novel col
29	206.8	24.9	1067	6	BD103305 Novel col
30	205	24.7	741	6	BD103341 Novel col
31	205	24.7	1269	6	BD103331 Novel col
32	202	24.3	663	6	BD103337 Novel col
33	202	24.3	1067	6	BD103306 Novel col
34	190	22.9	669	6	BD103339 Novel col
35	188	22.6	591	6	BD103329 Novel col
36	188	22.6	995	6	BD103335 Novel col
37	188	22.6	477	6	BD103304 Novel col
38	171.4	20.6	477	6	BD103334 Novel col
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40	154.8	18.6	246539	2	AC125638 Rattus no
41	153.6	18.5	147414	9	AC107953 Homo sapi
42	153.6	18.5	182475	2	AC023487 Homo sapi
43	151.6	18.2	175475	2	AC123631 Mus muscu
44	147.4	17.7	212049	5	EX005484 Zebrafish
45	111.6	13.4	151321	2	AC136264 Rattus no

ALIGNMENTS

RESULT 1
LOCUS AB002631
DEFINITION Homo sapiens mRNA for collectin 34, complete cds.
ACCESSION AB002631
VERSION AB002631.1 GI:5162874
KEYWORDS collectin 34.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Yamazaki,H.,
Keshi,H., Sakai,Y., Fukuh,A., Sakamoto,T. and Wakamiya,N.
Molecular cloning of a novel human collectin from liver (CL-L1)

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 QY 721 GACCCCTATGTCATAGGAGTGTGTGAGAGTGTGAGCTGTGAGCTGTGAGCTGTGAGATGGAATGACACA 780
 Db 726 GACCCCTATGTCATAGGAGTGTGTGAGAGTGTGAGCTGTGAGCTGTGAGATGGAATGACACA 785
 QY 781 GAGTCCCATCTTACATGTAATGTTCTGTGAGTTCATCAAGAGAAAAAG 831
 Db 786 GAGTCCCATCTTACATGTAATGTTCTGTGAGTTCATCAAGAGAAAAAG 836

RESULT 3
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 LOCUS AX376032 1016 bp DNA linear PAT 01-MAR-2002
 DEFINITION Sequence 99 from Patent WO0168848.
 ACCESSION AX376032
 VERSION AX376032.1 GI:19170408
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
 Zhang, Z.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 Patent: WO 0168848-A 99 20-SEP-2001;
 Genentech, Inc. (US)
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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FEATURES
 source

ORIGIN

Query Match 99.4%; Score 826.2; DB 6; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 4.7e-197;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGATGCTTGTGATCCTTCTCGAGAAACCAATTTATCTCTCTGGTACTATTCTT 60
 Db 22 ATGATGCTTGTGATCCTTCTCGAGAAACCAATTTATCTCTCTGGTACTATTCTT 81

QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTTGCC 120
 Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTTGCC 141
 QY 121 ACACACAAATTTCCACAGACCCCAAGGAGATGATGTGAAAAGGAGATCCAGAGAA 180
 Db 142 ACACACAAATTTCCACAGACCCCAAGGAGATGATGTGAAAAGGAGATCCAGAGAA 201
 QY 181 GAGGAAAGCATGCAAAAGTGGGACGATGGGCCGAAAGGAATTTAAAGAGAACTGGGT 240
 Db 202 GAGGAAAGCATGCAAAAGTGGGACGATGGGCCGAAAGGAATTTAAAGAGAACTGGGT 261
 QY 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCGAAAGGAATTTAAAGAGAACTGGGT 300
 Db 262 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCGAAAGGAATTTAAAGAGAACTGGGT 321
 QY 301 GGGGAAAAAGGTTTGTCTTGAATACCTGGAGAAAAAGGCAAGCAGTACTGTCTGTAT 360
 Db 322 GGGGAAAAAGGTTTGTCTTGAATACCTGGAGAAAAAGGCAAGCAGTACTGTCTGTAT 381
 QY 361 TGTGGAAGATACCGGAATTTGTTGGCACTGGGCCCTATAGTATTAGTATGTCCTGGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAATTTGTTGGCACTGGGCCCTATAGTATTAGTATGTCCTGGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC 501
 QY 481 TACATCTGTCAGGAAGAAGAACTACAGGAATTCCTAACCCACTGCAGGATTCGGGGT 540
 Db 502 TACATCTGTCAGGAAGAAGAACTACAGGAATTCCTAACCCACTGCAGGATTCGGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGACAGTAC 681
 QY 661 ATGTTTCAGACACACTCCACTGCAGACTATAGCACTGGAATGAGGGGAGGCCAGC 720
 Db 682 ATGTTTCAGACACACTCCACTGCAGACTATAGCACTGGAATGAGGGGAGGCCAGC 741
 QY 721 GACCCCTATGTCATAGGAGTGTGTGAGAGTCTGAGCTGTGAGATGGAATGACACA 780
 Db 742 GACCCCTATGTCATAGGAGTGTGTGAGAGTCTGAGCTGTGAGATGGAATGACACA 801
 QY 781 GAGTCCCATCTTACATGTAATGTTCTGTGAGTTCATCAAGAGAAAAAG 831
 Db 802 GAGTCCCATCTTACATGTAATGTTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 4
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 LOCUS AX359038 1016 bp mRNA linear PRI 03-OCT-2003
 DEFINITION Homo sapiens clone DN50980 COLEC10 (UNQ366) mRNA, complete cds.
 ACCESSION AX359038
 VERSION AX359038.1 GI:37183193
 KEYWORDS
 FLI CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1016)
 Clark, H.P., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hase, P.E.,
 Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,
 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,
 Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V.,
 Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wiesand, D., Woods, K.,

Matches 713; Conservative 0; Mismatches 117; Indels 0; Gaps 0;			
QY	1	ATGAATGGCTTTTCATCCTGCTTCGAAGAACAATTAATTCCTCCTGGTACTATTTCTT	60
Db	9	ATGAATGGCTTTTAGAGTCTCTGCTTCGAAGCAACCTATCCATGCTGTTGCTAGCTCTC	68
QY	61	TTGCAAAATTCAGAGCTGGCTGTGATATTCATAGCCGTCTACCGCTGAAGTCTGGCC	120
Db	69	TTGCACTTTACAGTCTGGCTGTGATGTTGATGTCATCAGCTGCAGAGTCTGTGCC	128
QY	121	ACACACACAAATTCACAGGACCCAAAGAGAGATGATGTTGAAAAGAGAGATCCAGAGAA	180
Db	129	ACACATACCAATTCACAGGACCTAAAGGGGATGATGTTGAAAGAGGTGACACAGAGAA	188
QY	181	GAGGGAAGCATGGCAAGTGGAGCGCATGGGCGGCGGAAGGAATTAAGGAGACTGGGT	240
Db	189	GAGGCAAGATGGCAAGTGGAGCGCCAGGAGCAAAAGAGGTGAAAGAGAGCTGGGT	248
QY	241	GATATGGGAGATCGGGGCAATATTGCGCAAGACTGGGCCATTTGGGAAGAAGGTTGACAAA	300
Db	249	GATATGGGAGCCAGGGTAATATTGSCAAGTCTGGCCCTATTGCAAGAAGGGTGACAAA	308
QY	301	GGGGAAGAGTTTCTTGGATCTACGAGAAAAGCAAGCAGGTACTGTCTGTGAT	360
Db	309	GGGGAAGAGGGTCTGCTTGGAAATCTCTGGAGAAAAGCAAGCAGGTACTGTGAT	368
QY	361	TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA	420
Db	369	TGTGCGAGTACCGGAAGTGGTTGGCACTGATATTAGTGTGCTGCTTTAGACA	428
QY	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGGATTAGGGAACCTGAAGAGAAATTTCTAC	480
Db	429	TCAATGAATTCATCAAGATGTTTATAGCAGGGATCCGGGAACTGAAGAGAAATTTCTAC	488
QY	481	TACATCGTCAGAGAGAGAACTACAGGGAATCCCTAACCCACTCGAGATTCGGGGT	540
Db	489	TACATTTGCGAGAGAGAGAACTACAGGGAATCTCTGACCCACTCGAGATCCGAGGA	548
QY	541	GGAATGTAGCATGCCCAAGATGAAGCTGCCAACACATCACTGCTGCTACTATGTTGCC	600
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QY	601	AAGAGTGGCTTTCTCGGGTGTTCATTCGCTGTGATGATCACTTGAAGGGAGGACAGTAC	660
Db	609	AGAGTGGTTCCTCAGAGTGTTCATTCGGGTCATGACCTTGAGGGAGGGGCGCATAT	668
QY	661	ATGTTTCACAGACACATCCATCGCAGAACTATAGCACTGGAATGAGGGGGAAACCCAGC	720
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QY	721	GACCCCTATGTCATGAGAGCTGTGGAGATGCTGAGCTTGGCAGATGGAATGACACA	780
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QY	781	GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAGAGAAAA	830
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DEFINITION AC080033			
ACCESSION AC080033.10			
VERSION GI:18767530			
KEYWORDS HTG.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1 (bases 1 to 141262)			
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.			
TITLE Homo sapiens chromosome 8, clone RP11-885J16			

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 141262)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P.,
FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRoque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G.,
Macdonald, P., Marquis, N., McCarty, M., McEwan, P., McKernan, K.,
McPheters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Tirell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (23-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 141262)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
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Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
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McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
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Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 141262)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A.,
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Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kanat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
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Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 20, 2002 this sequence version replaced gi:18653568.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center -----
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Center project name: L10939
 Center clone name: 885_J_16

FEATURES

source

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 6439. .6500
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 6950. .7186
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 complement (12616. .12915)
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 complement (13402. .13869)
 /rpt_family="MLT1C"
 complement (14079. .14128)
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 14318. .14351
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 15276. .15710
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 15711. .16021
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 15784. .15788
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 16152. .16207
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 /rpt_family="AT rich"
 complement (19159. .19244)

Query Match 46.9%; Score 390; DB 9; Length 141262;

Best Local Similarity 100.0%; Pred.No. 2.3e-87;

Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	442	GTGATAGCAGGATAGGAACTGAAGAGAAATCTACTACATCGTCGAGGAGAGAG	501
Db	55935	GTGATAGCAGGATAGGAACTGAAGAGAAATCTACTACATCGTCGAGGAGAGAG	55994
Qy	502	AACATACAGGAAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTAGCCATGCCCAAG	561
Db	55995	AACATACAGGAAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGCTAGCCATGCCCAAG	56054
Qy	562	GATGAAGTGCACACACACTCATCTGCTGATGTTGCCAGAGTGGCTTTTCGGGTG	621
Db	56055	GATGAAGTGCACACACACTCATCTGCTGATGTTGCCAGAGTGGCTTTTCGGGTG	56114
Qy	622	TTTCATGGCGTGAATGACCTTGAAGGGAGGAGGAGAGATGTTTCACAGACAACTCCCA	681
Db	56115	TTTCATGGCGTGAATGACCTTGAAGGGAGGAGGAGAGATGTTTCACAGACAACTCCCA	56174
Qy	682	CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGAC	741
Db	56175	CTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGCGACCCCTATGTCATGAGGAC	56234
Qy	742	TGTTGGAGATCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTAC	801
Db	56235	TGTTGGAGATCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTAC	56294
Qy	802	TTTGTCTGTGAGTTTCATCAAGAGAAAAAG	831

Db 56295 TTGTCTGTGAGTTCATCAGAGAAAAG 56324

RESULT 7

AC023487/c 182475 bp DNA linear HTG 26-MAR-2001

LOCUS Homo sapiens chromosome 8 clone RP11-164H21, WORKING DRAFT

DEFINITION SEQUENCE, 3 unordered pieces.

AC023487

ACCESSION AC023487

VERSION AC023487.10 GI:13357236

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 182475)

AUTHORS Abola, A.P., Bruno, D., Conn, L., Della Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Mao, J., Kemp, C., Kortler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelm, J., Yu, S., and Davis, R.W.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 182475)

AUTHORS Bruno, D., Conn, L., Della Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Yu, S., and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (14-FEB-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT On Mar 16, 2001 this sequence version replaced gi:13324778.

----- Genome Center

Center: Stanford DNA Sequencing and Technology Development

Center code: SOSTDC

Web site: <http://sequence-www.stanford.edu/group/human/>

Contact: hum-info@sequence.stanford.edu

----- Project Information

Center project name: 844

Center clone name: RP11-164H21

----- Summary Statistics

Sequencing Vector: M13mp18; X0513; 98% of reads

Chemistry: Dye-terminator; 0% of reads

Chemistry: Dye-terminator Big Dye; 99% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 180260 bases at least Q40

Consensus quality: 180441 bases at least Q30

Consensus quality: 180507 bases at least Q20

Insert size: 178614; agarose-fp

Insert size: 182275; sum-of-contigs

Quality coverage: 8.1x in Q20 bases; agarose-fp

Quality coverage: 7.9x in Q20 bases; sum-of-contigs.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 42072: contig of 42072 bp in length

* 42073 42172: gap of unknown length

* 42173 109254: contig of 67082 bp in length

* 109255 109354: gap of unknown length

* 109355 182475: contig of 73121 bp in length.

Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="8"

/clones="RP11-164H21"

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/note="assembly_name:Contig10"

109355..182475

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clone_end:SP6"

ORIGIN

Query Match 46.9%; Score 390; DB 2; Length 182475;

Best Local Similarity 100.0%; Pred. No. 2.2e-87; Indels 0; Gaps 0;

Matches 390; Conservative 0; Mismatches 0;

QY 442 GTGATAGCAGGGATTAGGAACTGAAGAGAAATTTCTACTACATCGTCGAGGAGAGAAG 501

DB 6233 GTGATAGCAGGGATTAGGAACTGAAGAGAAATTTCTACTACATCGTCGAGGAGAGAAG 6174

QY 502 AACTACAGGGAATCCCTAAACCCACTGCAGGATTCGGGTGGGAATGTAGCCATGCCCAAG 561

DB 6173 AACTACAGGGAATCCCTAAACCCACTGCAGGATTCGGGTGGGAATGTAGCCATGCCCAAG 6114

QY 562 GATGAAGCTGCCAACACACATCATCGTACTATGTTGCCAAGAGTGGCTTCTTTCCGGTG 621

DB 6113 GATGAAGCTGCCAACACACATCATCGTACTATGTTGCCAAGAGTGGCTTCTTTCCGGTG 6054

QY 622 TTCAATGCGGTGAATGACCTTGAAGAGGAGGAGGACAGTACATGTTTCACAGACATCCCA 681

DB 6053 TTCAATGCGGTGAATGACCTTGAAGAGGAGGAGGACAGTACATGTTTCACAGACATCCCA 5994

QY 682 CTGCAGAGCACTATACCAACTGGAATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741

DB 5993 CTGCAGAGCACTATACCAACTGGAATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5934

QY 742 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTAC 801

DB 5933 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTAC 5874

QY 802 TTTCTCTGTGAGTTCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831

DB 5873 TTTCTCTGTGAGTTCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5844

RESULT 8

AC097055 234922 bp DNA linear HTG 15-NOV-2002

LOCUS Rattus norvegicus clone CH230-2F22, WORKING DRAFT SEQUENCE, 3

DEFINITION Rattus norvegicus clone CH230-2F22, WORKING DRAFT SEQUENCE, 3

ACCESSION AC097055

VERSION AC097055.5 GI:25007102

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 234922)

AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Albrooks, S.L., Amaratunga, H.C., Aze, J.R., Ayele, M., Banks, T., Barbacia, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buay, C., Burck, F., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Chepel, Y., Colangelo, M., Collins, S., Collymore, A.,

REFERENCE
2 (pages 1 to 166900)
AUTHORS
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Baria, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepe, Y., Colanecio, M., Collins, S., Collymore, A.,

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* NORT: Estimated insert size may differ from sequence length
*       (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NORT: This is a 'working draft' sequence. It currently
*       consists of 3 contigs. The true order of the pieces
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Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Gidde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Kelle, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kulis, C., Lacroque, K., Lamazares, R.,
 Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McSwan, P., McKernan, K., Meldrim, J., Menes, L.,
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 Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
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 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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 Zainoun, J., Zembek, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 166900)

Birken, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
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 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fato, S.,
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 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kanat, A., Karatas, A., Kellis, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrim, J., Menes, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, R., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIER
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L24895
 Center clone name: 511_0_11

Sequencing vector: Plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 165673 bases at least Q40
 Consensus quality: 166156 bases at least Q30
 Consensus quality: 166365 bases at least Q20
 Insert size: 157000; agarose-ff
 Insert size: 166600; sum-of-contigs
 Quality coverage: 13.2 in Q20 bases; agarose-ff
 Quality coverage: 12.4 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 4 contigs. Gaps between the contigs
 are represented as runs of N. The order of the pieces
 is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

1 48320: contig of 48320 bp in length
 48321 48420: gap of 100 bp
 48421 59799: contig of 11379 bp in length
 59800 59899: gap of 100 bp
 59900 135830: contig of 75931 bp in length
 135831 135930: gap of 100 bp
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ORIGIN

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 Best Local Similarity 87.9%; Pred. No. 3.4e-68;
 Matches 342; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 442 GTGATGACGGGATTAGGGAACCTGGAAGAGAAATTTACTACATCGTGCGAGGAGAGAG 501
 Db 15148 GTTATAGCAGGATCCGGGAATCTGAAGAGAAATTTACTACATTTGTGCGAGGAGAGAG 15207
 QY 502 AACTACAGGGAATCCCTAACCCACTCCAGATTCGGGGTGGGAATCTAGCCATGCCCAAG 561
 Db 15208 AACTACAGGGAATCTCTGACCCACTCCAGATCCGAGGAGGATGCTAGCCATGCCCAAG 15267
 QY 562 GATGAGCTCCCAACACATCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTTCGGGTG 621
 Db 15268 GATGAGTCTGTTAACACCCCTTATGCTGACTATGTCGCAAGAGTGGTTTCTTCAGAGTG 15327
 QY 622 TTCAATGGCTGATGATGACCTTGAAAGGGGAGGACAGTACATGTTTACAGACAACTCCA 681
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 Db 15388 TTGAGAACTATAGCACTGGAATGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15447
 QY 742 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGGCATCTTACCATTGAT 801
 Db 15448 TGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGGCATCTTACCATTGAT 15507
 QY 802 TTTGTTCTGTGAGTTTCATCAAG 830
 Db 15508 TTTGTTCTGTGAGTTTCATCAAG 15536

RESULT 10
 AC123656
 LOCUS AC123656 Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered
 DEFINITION pieces.
 ACCESSION AC123656
 VERSION AC123656.6 GI:29294284

HTG; HTGS PHASE1; HTGS_DRAFT.
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 222510)
 Biren, B., Nusbaum, C. and Lander, E.
 Mus musculus, clone RP23-188W21
 Unpublished
 2 (bases 1 to 222510)
 Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
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 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,
 Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
 Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
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 O'Neil, D., Oliver, J., Peterson, C. H., O'Connor, T., O'Donnell, P.,
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 Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
 Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testfaye, S.,
 Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 222510)
 Biren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,
 Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
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 Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, B., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, J., Peterson, C., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
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 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 27, 2003 this sequence version replaced gi:28626969.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L26354
 Center clone name: 188 M 21
 ----- Summary Statistics
 Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 221635 bases at least Q40
 Consensus quality: 221908 bases at least Q30
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 Insert size: 200000; agarose-fp
 Insert size: 222010; sum-of-contigs
 Quality coverage: 10.7 in Q20 bases; agarose-fp
 Quality coverage: 9.6 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1 2031: contig of 2031 bp in length
 * 2032 2131: gap of 100 bp
 * 2132 15244: contig of 13113 bp in length
 * 15245 15344: gap of 100 bp
 * 15345 37649: contig of 22305 bp in length
 * 37650 37749: gap of 100 bp
 * 37750 148102: contig of 110353 bp in length
 * 148103 148202: gap of 100 bp
 * 148203 190361: contig of 42159 bp in length
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 * Best Local Similarity 87.9%; Pred. No. 3.3e-68;
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 * 442 GTGATGACGAGGATTTAGGAACTGAGAGAAATCTACTACTATCTGTCAGAGAGAG 501
 * 157200 GTTATAGCAGGATTCGGGAAATCTAGAGAAATTTCTACTATGTCAGGAGAG 157259
 * 502 AACTACAGGAAATCCCTAAACCCACTGCAGATTCGGGGTGGAAATCTAGCCATGCCCAAG 561
 * 157260 AACTACAGGAAATCTCTGACCCACTGCAGATTCGGAGGAGGATGCTAGCCCAAG 157319
 * 562 GATGAGCTCCACACACTCATCGCTGACTATGTCAGAGAGTGGCTTTTCGGGTG 621
 * 157320 GATGAGCTGTTAACCCCTTATGCTGACTATGTCGCGAGAGTGGTTTCTCAGAGTG 157379
 * 622 TTCAATGGCGCTGAATGACCTTGAAGGGGAGGACAGTACATGTTTCACAGACAACTCCA 681
 * 157380 TTCAATGGCGCTGAATGACCTTGAAGGGGAGGAGGAGTATGTTTTCACAGATAACTCCA 157439
 * 682 CTGCAGACTATAGCACTGGATGAGGGGGACCCAGCGACCCCTATGCTCATGAGAC 741

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

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Db      157440 TTGCAGAACTACAGCAACTGGAAGAGGAGGAGCACTAGTACCCTCGGCGCATGAGGAC 157499
Qy      742   TGTGTGGATGCTGAGCTCTGGAGATGGATGACACAGAGTGCCATCTTACCATGTAC 801
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RESULT 11
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LOCUS   AC131337.4 GI:30017797
DEFINITION Mus musculus clone RP23-480E1, WORKING DRAFT SEQUENCE, 17 unordered
pieces.
ACCESSION AC131337
VERSION   AC131337.4
KEYWORDS  HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345420)
Birren,B., Nusbaum,C. and Lander,B.
Mus musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chararo,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
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Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
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Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome

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COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 17, 2003 this sequence version replaced gi:28626850.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L26504
 Center clone name: 480_E_1

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 17 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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* 7232 7331: gap of 100 bp
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* 13581 13680: gap of 100 bp
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* 24246 24345: gap of 100 bp
* 24346 33304: contig of 8959 bp in length
* 33305 33404: gap of 100 bp
* 33405 43959: contig of 10555 bp in length
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* 166938 167037: gap of 100 bp
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Best Local Similarity 87.9%; Pred. No. 3.3e-68;
Matches 342; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy 562 GATGAAGCTGCCAACACACTCATCGTCTACTATGTTGCCAAGAGTGGTCTTTTGGGGT 621
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Qy 622 TTCTATGGCTGATGATGACCTTGAAGAGGAGGAGCAGTACATGTTTACAGACACACTTCCA 681
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RESULT 12
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DEFINITION Xenopus laevis collectin sub-family member 11, mRNA (cdna clone
ACCESSION MGC:69012 IMAGE:4963954), complete cds.
VERSION BC056052
KEYWORDS MGC.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.

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REFERENCE
AUTHORS Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.,
and Richardson,P.
TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)
MEDLINE 22341132
PUBMED 12454917
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Klauser,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marudina,K., Farmer,A.S., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Uddin,T.B., Toehiyuki,S.,
Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.U., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shevchenko,Y.,
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Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE
AUTHORS Klein,S. and Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20852-7510, USA
REMARK NIH-MGC Project
COMMENT Contact: XGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLUM)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLUM at: http://image.llnl.gov
Series: IRAC Plate: 129 Row: 1 Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein.
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DB 225 CTGGTCTGAAGGAGATCCGCGAGAAAAGGAGAGAAAGAGCTCCAGGAGAGACCGGAA 284
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DB |||||
DB 285 GAGTTGGCCCTCTGGGAAAGGAGAAATGGCGATAAGGAATAAAGGAAGCATGG 344
QY 257 GCAATATTGGCAAGACTGGGCCATTGGAGAAAGGAGTGAACAAAGGGGAAAAAGTTTG 316
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DB 345 GTCGTCATGGAAGATTGTCCTATTGTTGTCGAAGGTGAAGAGGGGAGTTGTTGTCAG 404
QY 317 TTGGAATACCTGGAGAAAAGGCAAGGAGTACTGTCTGTGATGTGGAGATCCGGA 376
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DB 405 TCGGCCCTCCAGGACCAATGGAGAGCCAGGAATCCCTGTGATGTGGACAGCTAAGAA 464
QY 377 AATTTGTTGGCAACTGATATTAGTATTGCCCGCTCAAGACATCTATGAAGTTGTGA 436
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QY 437 AGAATGTGATAGCGGATTAAGGAACTAAGAGAAATTTCTACTACATCGTGCAGGAAG 496
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DB 525 AAAATGTTGTTGCTGGAGTGGAGAGACGAGACAAAAATCTATCTTCTGGTGAAGGAAG 584
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.
Wakamiya,N., Keshi,H., Otani,K., Sakamoto,T. and Kishi,Y.
Patent: WO 0181401-A 31 01-NOV-2001;
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA,HIROYUKI
KESHI, KATSUKI OTANI,TAKASHI SAKAMOTO,YUICHIRO KISHI
OS Homo sapiens (human)
PN WO 0181401-A/31
PD 01-NOV-2001
PF 23-APR-2001 WO 2001JP003468
PR 21-APR-2000 JP 00P 120358
PI NOBUTAKA WAKAMIYA,HIROYUKI KESHI,KATSUKI OTANI,TAKASHI PI
SAKAMOTO,
PI YUICHIRO KISHI
PC C07K14/47,C12N15/12,C12P21/02,A01K67/027,C07K16/18,G01N33/53
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DB 83 CTGGGATGAGCGCTGCTCTGCAGATCCTCGTCCCTGGCCCTCAAGGGGATCGGGAG 142
QY 161 AAAAGAGATCCAGGAGAGAGGAAAAGCATGGCAAAGTGGGACGATCGGGCCGAAAG 220
DB |||||
DB 143 AGAAGGAGACAAAGGCGCCCGGACGGCTTGAAGAGTCCGCCCCCACGGGAGAAAAAG 202
QY 221 GAATTAAGGAGAACTGGGTGATATGGAGATCGGGCAATATTGGCAAGCTGGGCCCA 280
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DB 203 GAGACATGGGGGCAAAAGGACAGAAAGGAGTGTGGTCTGATGGAATAATTTGGTCCA 262
QY 281 TTGGAAGAGAGGGTGAACAAAGGGGAAAAAGTTTGTGGGAATATCTGGAGAAAAAGCA 340
DB |||||
DB 263 TTGGCTCTAAAGGTGAAGAAAGAGATTCGGTGCATAGGACCCCTGCTCTTAATGGAG 322
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QY 521 CCCACTGCAGGATTCGGGGTGGAAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACAC 580
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581 TCATCGCTGACTATGTTGCCAGAGTGGCTTTCTTCGGGTGTTCTATTGGCGTGAATGACC 640
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641 TTGAAAGGGAGGACAGTACATGTTTCCAGACAAACACTCCACTGACAGAACTATAGCAACT 700
623 TGAGAGAGGAGGCGCGCTTTCGTGTACTCTGTGACCACTCCCCCATGCGGACCTTCAACAGT 682
701 GGAATGAGGGGAGACCCAGGACCCCTATATGTCATGAGGACTGTGTGAGATGCTGAGCT 760
683 GCGCGACGGTGAAGCCCAACAATGCTACGACGAGGAGGACTGCGGTGAGATGCTGCGCT 742
761 CTGCGCAGATGGAATGACACAGAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCA 820
743 CGGCGGCTGGAACGAGCGTGGCTGCCACACCACTGACTTCTCATGTGTGAGTTGACA 802
821 AGAAGAAAAG 831
803 AGGAGAACATG 813

RESULT 14
AR252616
LOCUS 1238 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 356 from patent US 6478825.
ACCESSION AR252616
VERSION AR252616.1 GI:27300524
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 1238)
AUTHORS Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 356 12-NOV-2002;
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source Location/Qualifiers
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/organism="unknown"

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Query Match 29.4%; Score 244.6; DB 6; Length 1238;
Best Local Similarity 58.4%; Pred. No. 1.1e-50;
Matches 427; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 101 CTACCGCTGAAGTCTGTGCCACACACAAATTTCCAGGACCCCAAGAGATGATGGT 160
DB 149 CTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGAGCTCAAGGGGATCGGGAG 208
QY 161 AAAAAGGAGATCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 220
DB 209 AGAAGGAGAGCAAAAGGGGCGCCCGGACGGCTGGAAGAGTCCGCCCCACGGGAGAAAAG 268
QY 221 GAATTAAGGAGAACTCGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTCGGCCCA 280
DB 269 GAGACATGGGGGCAAAAGGACAGAAAGGACAGTGTGGTGTGCTCATGAAATAATGGTCCA 328
QY 281 TTGGAAGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 340
DB 329 TTGGCTCTAAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 388
QY 341 AAGCAGTACTGTCTGTGATTTGGAGATATCGGAAATTTTGGCACTATGATATTA 400
DB 389 AACGAGCCCTCCCATGTGATGTCAGCAGCTCGCAAGGCCATCGGGAGATGACCAACC 448
QY 401 GTATTGCCCGCTCAGACATCTATGAAGTTTGTCAAGATTTGATAGAGGATTTAGG 460
DB 449 AGGTCTCTAGCTGACCGAGCTCAAGTTCATCAAGATGCTGTGTCGCGGTGTGCGG 508
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DB 509 AGACGGAGGACAGATCTACCTGCTGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 568
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QY 521 CCCACTGCAGGATTCGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAC 580
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DB 623 TGATGCGCGCATACCTGGGCGCAAGCGGCTTGGCCCGTGTCTTTCATCGGCATCAACGACC 688
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QY 701 GGAATGAGGGGAGACCCAGGACCCCTATATGTCATGAGGACTGTGTGAGATGCTGAGCT 760
DB 749 GCGCGACGGTGAAGCCCAACAATGCTACGACGAGGAGGACTGCGGTGAGATGCTGCGCT 808
QY 761 CTGCGCAGATGGAATGACACAGAGTGCATCTTACCATGTACTTGTCTGTGAGTTCATCA 820
DB 809 CGGCGGCTGGAACGAGCGTGGCTGCCACACCACTGACTTCTCATGTGTGAGTTTGACA 868
QY 821 AGAAGAAAAG 831
DB 869 AGGAGAACATG 879

RESULT 15
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LOCUS 1238 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 356 from Patent WO0073454.
ACCESSION AX403469
VERSION AX403469.1 GI:21436970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1.
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D., Ferrar, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;
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source Location/Qualifiers
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ORIGIN
Query Match 29.4%; Score 244.6; DB 6; Length 1238;
Best Local Similarity 58.4%; Pred. No. 1.1e-50;
Matches 427; Conservative 0; Mismatches 304; Indels 0; Gaps 0;

QY 101 CTACCGCTGAAGTCTGTGCCACACAAATTTCCAGGACCCCAAGGAGATGATGGT 160
DB 149 CTGGCGATGACGCTGCTCTGTGCAGATCCTCGTCCCTGAGCTCAAGGGGATCGGGAG 208
QY 161 AAAAAGGAGATCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 220
DB 209 AGAAGGAGAGCAAAAGGGGCGCCCGGACGGCTGGAAGAGTCCGCCCCACGGGAGAAAAG 268
QY 221 GAATTAAGGAGAACTCGGTGATATGGGAGATCGGGGCAATATTTGGCAAGACTCGGCCCA 280
DB 269 GAGACATGGGGGCAAAAGGACAGAAAGGACAGTGTGGTGTGCTCATGAAATAATTTGGTCCA 328
QY 281 TTGGAAGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 340
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Db	449	AGGTCTCT	CAGCTG	ACCGAG	CTCAAG	TTCA	TCA	TCA	TCA	508
QY	461	AAACTGA	AGAGAA	TTCTACT	ATCAT	CTGTG	CAAG	AGAGAA	CTACAGG	520
Db	509	AGACCGA	GAGCAAG	ATCTAC	CTGCTG	GTGAA	AGAG	AGAG	AGAG	568
QY	521	CCCACTG	TCAGG	ATTCGG	GTGGA	ATGCT	AGCC	ATGCA	AGCTG	580
Db	569	TGTCCTG	CCAGG	CGCGG	GGGAC	GGCTG	AGC	ATG	CCNAG	628
QY	581	TCATCGT	GA	CTATG	TGCA	AGAG	TGG	CTTCT	TTGCGG	640
Db	629	TGATGCC	CGCAT	ATCCTG	CGCA	AGCG	CGCTG	GGCC	GTGCTT	688
QY	641	TTGAAAG	GAGG	GCAG	ATAC	ATGTT	TCAG	ACA	CACTCC	700
Db	689	TGGAGAG	GAGG	CGCCTT	CGTGT	ACTCT	GAC	CTCC	ATCC	748
QY	701	GGAATG	AGGGG	AAAC	CCAG	CCCTA	TG	TCAT	GAG	760
Db	749	CGCGCAG	CGGTG	AGCCCA	CAATG	CTTAC	GAC	AGAG	AGG	808
QY	761	CTGGCAG	ATGGA	TGAC	ACAG	AGTGC	CA	CTTAC	CATG	820
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QY	821	AGAAGAA	AAAG	831						
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 Job time : 3309 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:43:17 ; Search time 398 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: Geneseqn2001bs.*

6: Geneseqn2002s.*

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9: Geneseqn2003cs.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	826.2	99.4	1016	2	AAz233973	Human PRO
3	826.2	99.4	1016	3	AAz78480	Human PRO
4	826.2	99.4	1016	4	AAa45974	Human DNA
5	826.2	99.4	1016	7	ABx78577	Human PRO
6	826.2	99.4	1016	7	ABx78577	Human PRO
7	826.2	99.4	1016	7	ACA71029	Novel hum
8	826.2	99.4	1016	7	ACC87557	Human sec
9	826.2	99.4	1016	7	ACC87557	Human sec
10	826.2	99.4	1016	7	ACD04116	Human sec
11	826.2	99.4	1016	7	ACA69447	cdNA enco
12	826.2	99.4	1016	7	ACA90292	Novel hum
13	826.2	99.4	1016	7	ACC89399	Human sec
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15	826.2	99.4	1016	7	ACA93832	Human sec
16	826.2	99.4	1016	7	ACD15225	Human sec
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ALIGNMENTS

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OS Homo sapiens.
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FH Key Location/Qualifiers
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XX
PN WO9937767-Al.
XX
PD 29-JUL-1999.
XX
PF 24-JUL-1998; 98WO-JP003328.
XX
PR 23-JAN-1998; 98JP-00011281.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI: 1999-458691/38.
XX
DR F-PSDB; AAY25518.
XX
PT New collectin protein of human origin and DNA encoding it.
XX
PS Claim 2; Page 39-42; 58pp; Japanese.
XX
CC This invention describes the isolation and characterisation of a novel human collectin protein and its encoding polynucleotide. The human collectin exhibits antibacterial and antiviral activity and can be used as an agent for the treatment of human bacterial and viral infections.
XX
CC This sequence encodes the novel human collectin
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SQ Sequence 1595 BP; 444 A; 322 C; 382 G; 447 T; 0 U; 0 Other;

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Best Local Similarity		100.0%; Pred. No. 1.4e-242;
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RESULT 2
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AC AAZ33973;
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DT 07-DEC-1999 (first entry)
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DE Human PRO702 nucleotide sequence.
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secreted protein; transmembrane protein; ss.		
Homo sapiens.		
MO9946281-A2.		
16-SEP-1999.		
XX	08-MAR-1999;	99WO-US005028.
PF	10-MAR-1998;	98US-0077450P.
XX	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077641P.
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PR	13-MAR-1998;	98US-0078004P.
PR	17-MAR-1998;	98US-00040220.
PR	20-MAR-1998;	98US-0078886P.
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PR	09-APR-1998;	98US-0081195P.
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 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 PR (GETH) GENENTECH INC.
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 PI WPI; 1999-551358/46.
 DR P-PSDB; AAY41698.
 DR
 PR New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 PR
 PR Claim 2; Fig 36; 530pp; English.
 PR
 PR The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders.
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AAY41774 represents polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention
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 CC Query Match 99.4%; Score 826.2; DB 2; Length 1016;
 CC Best Local Similarity 99.6%; Pred. No. 3.2e-241;
 CC Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Qy 361 TGTGGAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCCCGCTCAAGACA 420
 Db 382 TGTGGAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCCCGCTCAAGACA 441
 Qy 421 TCTATGAAGTTTCTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTCTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAATTTCTAC 501
 Qy 481 TACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
 Db 502 TACATCGTCGAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
 Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACAACACTCATCGCTGACTATTTGCC 621
 Qy 601 AAGATGGCTTCTTTCGGGTGTTTCATTCGCGTGAATGACCTTGAAGGGAGGAGCAGTAC 660
 Db 622 AAGATGGCTTCTTTCGGGTGTTTCATTCGCGTGAATGACCTTGAAGGGAGGAGCAGTAC 681
 Qy 661 ATGTTTCACAGACAACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC 720
 Db 682 ATGTTTCACAGACAACACTCCACTGCAGAACTATAGCACTGGAATGAGGGGAAACCCAGC 741
 Qy 721 GACCCCTATGCTCATGAGCACTGTTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGCTCATGAGCACTGTTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 Qy 781 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAAGAAAAAG 831
 Db 802 GAGTGCCATCTTACCATGTACTTGTCTGTGAGTTTCATCAAGAAAGAAAAAG 852
 DE
 DE Human PRO702 (UNQ366) nucleotide sequence SEQ ID NO:96.
 DE
 DE Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
 DE expressed sequence tag; detection; cancer; ss.
 OS Homo sapiens.
 OS
 OS WO200053756-A2.
 FN
 FN 14-SEP-2000.
 PD
 PD 18-FEB-2000; 2000WO-US004341.
 PF
 PF 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 29-MAR-1999; 99US-0126773P.
 PR 21-APR-1999; 99US-0130232P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tunas D, Williams PM, Wood WI;
 XX WPI; 2000-611443/58.
 DR P-PSDB; AAB44254.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods, to
 PT target bioactive molecules to specific cells, and to modulate cellular
 PT activities.
 XX
 PS Claim 2; Fig 36; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences
 XX
 SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
 Query Match 99.4%; Score 926.2; DB 3; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 3.2e-241;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 ATGATGGCTTGGATCCTCTCTCGAGAAACCAATTTATCTCTGTTACTATTCTT 60
 22 ATGATGGCTTGGATCCTCTCTCGAGAAACCAATTTATCTCTGTTACTATTCTT 81
 61 TTGCAAAATTCAGAGTCTGGGTCCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGC 120
 82 TTGCAAAATTCAGAGTCTGGGTCCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGC 141
 121 ACACACAAATTCACGAGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
 142 ACACACAAATTCACGAGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 201
 181 GAGGGAAGAGATGCGCAAGTGGGACGATCGGGCCGGAAGGAATTAAGAGAGAACTGGGT 240
 202 GAGGGAAGAGATGCGCAAGTGGGACGATCGGGCCGGAAGGAATTAAGAGAGAACTGGGT 261
 241 GATATGGAGATCGGGGCAATATTGGCAAGTGGGCGCCATTGGGAAGAGAGTGAACA 300
 262 GATATGGAGATCGGGGCAATATTGGCAAGTGGGCGCCATTGGGAAGAGAGTGAACA 321
 301 GGGGAAAAGTTTCTTGGGAATACCTGGGAAAAGCAAGCAGTACTGTCTGTGAT 360
 322 GGGGAAAAGTTTCTTGGGAATACCTGGGAAAAGCAAGCAGTACTGTCTGTGAT 381
 361 TGTGGAAGATCCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGGCTCAAGACA 420
 382 TGTGGAAGATCCGGAATTTGTTGGCAACTGATATTAGTATTCGCCGGCTCAAGACA 441
 421 TCTATGAATTTGTCAGAAATGTCATAGCAGGATTAGGGAATCAAGAGAAATTTCTAC 480
 442 TCTATGAATTTGTCAGAAATGTCATAGCAGGATTAGGGAATCAAGAGAAATTTCTAC 501

QY 481 TACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 540
 DB 502 TACATCGTGCAGGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTACTATGTTGCC 600
 DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTACTATGTTGCC 621
 QY 601 AAGAGTGGCTCTTTTCGGGTGTTTCATTTGCGTGAATGACCTTGAAGGAGGACAGTAC 660
 DB 622 AAGAGTGGCTCTTTTCGGGTGTTTCATTTGCGTGAATGACCTTGAAGGAGGACAGTAC 681
 QY 661 ATGTTTCAAGACAACTCCACTGCGAGACTATAGCACTGGAATGAGGGGAAACCCAGC 720
 DB 682 ATGTTTCAAGACAACTCCACTGCGAGACTATAGCACTGGAATGAGGGGAAACCCAGC 741
 QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATGGAATGACACA 780
 DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATGGAATGACACA 801
 QY 781 GAGTGGCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 831
 DB 802 GAGTGGCATCTTACCATGTACTTTGCTGTGAGTTTCATCAAGAGAAAAAG 852
 RESULT 4
 AAS45974
 ID AAS45974 standard; cDNA; 1016 BP.
 AC AAS45974;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DS Human DNA encoding PRO polypeptide sequence #50.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor; alpha; TNF-alpha; colon;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; liver;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.
 XX
 OS Homo sapiens.
 XX
 XX WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US0006520.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186968P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032878.
 PR 20-DEC-2000; 2000WO-US034956.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-602746/68.
 DR P-PSDB; AAU29073.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 2; Fig 99; 774pp; English.
 XX
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells; whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 SQ Sequence 1016 BP; 312 A; 197 C; 261 G; 246 T; 0 U; 0 Other;
 Query Match 99.4%; Score 826.2; DB 4; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 3.2e-241;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 2Y 1 ATGAATGGCTTTGGCATCTTCTTCGGAAGAAACCAATTATCTCTCTGGTACTATTCTT 60
 DB 22 ATGAATGGCTTTGGCATCTTCTTCGGAAGAAACCAATTATCTCTCTGGTACTATTCTT 81
 2Y 61 TTGCAAAATTCAGATCTGGGTCTGGATTTGATAGCGGCTCTACCCCTGAAGTCTGTGCC 120
 DB 82 TTGCAAAATTCAGATCTGGGTCTGGATTTGATAGCGGCTCTACCCCTGAAGTCTGTGCC 141
 2Y 121 ACACACAAATTTACACAGGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGGAGAA 180
 DB 142 ACACACAAATTTACACAGGACCCCAAGAGAGATGATGGTGAAGAGAGATCCAGGAGAA 201
 2Y 181 GAGGGAAGAGATGGCAAGTGGGACGATGGGCGCGAAGAGAAATTAAGAGAACTGGGT 240
 DB 202 GAGGGAAGAGATGGCAAGTGGGACGATGGGCGCGAAGAGAAATTAAGAGAACTGGGT 261
 2Y 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCGCGAAGAGAGAGTGCACAA 300
 DB 262 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCGCGAAGAGAGAGTGCACAA 321

QY 301 GGGGAAAAGGTTTGGCTTGGAAATACCTGGAGAAAAAGGCAAGAGTACTGTCTGTGAT 360
 DB 322 GGGGAAAAGGTTTGGCTTGGAAATACCTGGAGAAAAAGGCAAGAGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGGCTCAAGACA 420
 DB 382 TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATAGGGAACCTCAAGAGAAATTTCTAC 480
 DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGAATAGGGAACCTCAAGAGAAATTTCTAC 501
 QY 481 TACATCTGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGACAGGATTTGGGGT 540
 DB 502 TACATCTGTCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGACAGGATTTGGGGT 561
 QY 541 GGAATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 600
 DB 562 GGAATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 621
 QY 601 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
 DB 622 AAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 681
 QY 661 ATGTTCCACAGACAACTCCACTGCAAGAACTAGCAACTGCAAGTGAAGAGGAGGAGGAGGAG 720
 DB 682 ATGTTCCACAGACAACTCCACTGCAAGAACTAGCAACTGCAAGTGAAGAGGAGGAGGAGGAG 741
 QY 721 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGGAGATGGAATGACACA 780
 DB 742 GACCCCTATGCTATGAGGACTGTGTGGAGATGCTGAGCTCTGGGAGATGGAATGACACA 801
 QY 781 GAGTGGCATCTTACCATTGCTTGTCTGTGAGTTCATCAAGAGAAAAAG 831
 DB 802 GAGTGGCATCTTACCATTGCTTGTCTGTGAGTTCATCAAGAGAAAAAG 852
 RESULT 5
 ABX78577
 ID ABX78577 standard; cDNA; 1016 BP.
 AC ABX78577;
 XX 15-APR-2003 (first entry)
 DT Human PRO polynucleotide #50.
 DE Human PRO polynucleotide #50.
 XX
 KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
 KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy.
 XX
 OS Homo sapiens.
 PN US2003027272-A1.
 PD 06-FEB-2003.
 XX
 PF 21-JUN-2002; 2002US-00176492.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.


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PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101923P.
PR 25-SEP-1998; 98US-0101786P.
PR 25-SEP-1998; 98US-0102207P.
PR 25-SEP-1998; 98US-0102240P.
PR 25-SEP-1998; 98US-0102330P.
PR 25-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 01-OCT-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match          99.4%; Score 826.2; DB 7; Length 1016;
Best Local Similarity 99.6%; Pred No. 3.2e-241;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAATGGCTTTGCAATCTCTGCTTTCGAGAAACCAATTTATCTCTCGTGACTATTTCTT 60
22 ATGAATGGCTTTGCAATCTCTGCTTTCGAGAAACCAATTTATCTCTCGTGACTATTTCTT 81
61 TTGCAAAATTCAGAGTCTGGTCTGATATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
82 TTGCAAAATTCAGAGTCTGGTCTGATATTTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
121 ACACACAAATTTACAGGACCCAAAGAGATGATGTTGAAAAGAGATGCCAGGAGAA 180
142 ACACACAAATTTACAGGACCCAAAGAGATGATGTTGAAAAGAGATGCCAGGAGAA 201
181 GAGGGAAGCATGGCAAGTGGGAGCGCATGGGCGGAAGCAATTAAGGAGACTGGT 240
202 GAGGGAAGCATGGCAAGTGGGAGCGCATGGGCGGAAGCAATTAAGGAGACTGGT 261
241 GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 300
262 GATATGGGAGATCGGGGCAATATTCGCAAGACTGGGCCCATTTGGGAAGAGGGTGACAAA 321
301 GGGGAAAAGGTTTCTTGGATATCTGAGAAATACCTGGAGAAAAGCAAGCAGTCTGTGTAT 360
322 GGGGAAAAGGTTTCTTGGATATCTGAGAAATACCTGGAGAAAAGCAAGCAGTCTGTGTAT 381
361 TGTGGAAGATACCGGAAATTTCTTGGACAACTGGATATTAGTATTCGCCGCTCAAGACA 420
382 TGTGGAAGATACCGGAAATTTCTTGGACAACTGGATATTAGTATTCGCCGCTCAAGACA 441
421 TCTATGAAGTTTGTCAAGATGTGTAGCAGGATATGGGAAATCTGAAGAGAAATTTCTAC 480
442 TCTATGAAGTTTGTCAAGATGTGTAGCAGGATATGGGAAATCTGAAGAGAAATTTCTAC 501
481 TACATCGTCCAGAGAGAGAACTACAGGAAATCCCTTAACCCACTGCAGATTCGGGGT 540
502 TACATCGTCCAGAGAGAGAACTACAGGAAATCCCTTAACCCACTGCAGATTCGGGGT 561
541 GGAATGCTAGCAATGCCCAAGATGAAGCTGCCAAACACATCATCTGCTGATATGTGCC 600
562 GGAATGCTAGCAATGCCCAAGATGAAGCTGCCAAACACATCATCTGCTGATATGTGCC 621
601 AAGAGTGGCTTTCTTGGGTGTTTCAATTCGCTGATGACCTTGAAGAGGAGGACAGTAC 660
622 AAGAGTGGCTTTCTTGGGTGTTTCAATTCGCTGATGACCTTGAAGAGGAGGACAGTAC 681
661 ATGTTCCACAGACAACTCCACTGACAGAACTATAGCAACTGGAAATAGGGGGAAACCCAGC 720
682 ATGTTCCACAGACAACTCCACTGACAGAACTATAGCAACTGGAAATAGGGGGAAACCCAGC 741
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QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCATGCTACTTTGTCTGTGAGTTCATCAAGAGAAAAAG 831
DB 802 GAGTGCCATCTTACCATGCTACTTTGTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 6
ACA75549
ID ACA75549 standard; cDNA; 1016 BP.
XX
AC ACA75549;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO702 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
PF 26-JUN-2002; 2002US-00183012.
XX
18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0083120P.
PR 24-OCT-1997; 97US-0083121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063546P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0083870P.
PR 31-OCT-1997; 97US-0084103P.
PR 13-NOV-1997; 97US-0055311P.
PR 21-NOV-1997; 97US-0056120P.
PR 24-NOV-1997; 97US-0056466P.
PR 24-NOV-1997; 97US-0056772P.
PR 11-DEC-1997; 97US-0059335P.
PR 12-DEC-1997; 97US-0059425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079684P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
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Db 22 ATGATGGCTTTGGATCTCTTGCATGAAAGAACCAATTTATCTCTCGTACTATTTCTT 81
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 Db 82 TTGCAAAATTCAGAGTCGTGGTCTGATATGATACCGCTCTACCGTGAAGTCTGTGCC 141
 QY 121 ACACACACAAATTCACAGGACCCAAAGAGATGATGTAAGAGAGATGATGTAAGAGAG 180
 Db 142 ACACACACAAATTCACAGGACCCAAAGAGATGATGTAAGAGAGATGATGTAAGAGAG 201
 QY 181 GAGGAAAGCATGGCAAGTGGGACGCTAGGAGGAGGAAATTAAGAGAGATGCGGT 240
 Db 202 GAGGAAAGCATGGGACGCTAGGAGGAGGAAATTAAGAGAGATGCGGT 261
 QY 241 GATATGGGAGATCGGGGCAATATGGCAAGCTGGGCCCCATGGGAGAGAGGATGACAA 300
 Db 262 GATATGGGAGATCGGGGCAATATGGCAAGCTGGGCCCCATGGGAGAGAGGATGACAA 321
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 Db 322 GGGGAAAAGGTTTCTTGGATACCTGAGAGAAAGCAAGCAGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAATTTGTTGGACAACTGGATATGATGTCGCCGCTCAGACA 420
 Db 382 TGTGGAAGATACCGGAATTTGTTGGACAACTGGATATGATGTCGCCGCTCAGACA 441
 QY 421 TCTATGAAAGTTTGTCAAGAATGTGATAGCAGGATAGGGAAGCAAGCAAGAAATTTCTAC 480
 Db 442 TCTATGAAAGTTTGTCAAGAATGTGATAGCAGGATAGGGAAGCAAGCAAGAAATTTCTAC 501
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 Db 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
 QY 541 GGAATGCTAGCATCCCAAGAGTGAAGCTGCCAACAACATCATCGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCATCCCAAGAGTGAAGCTGCCAACAACATCATCGCTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTTTCGGGTGTTTCAATGGCTGTGAATGACCTTGAAGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTTTTCGGGTGTTTCAATGGCTGTGAATGACCTTGAAGGAGGACAGTAC 681
 QY 661 ATGTTTCACAGACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
 Db 682 ATGTTTCACAGACACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
 QY 721 GACCCCTATGTTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA 780
 Db 742 GACCCCTATGTTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGCGAGATGGAATGACACA 801
 QY 781 GAGTCCCATCTTACCATGCTATTTGTTGAGTTCATCAAGAGAAAG 831
 Db 802 GAGTCCCATCTTACCATGCTATTTGTTGAGTTCATCAAGAGAAAG 852

RESULT 7
 ACA71029
 ID ACA71029 standard; cDNA; 1016 BP.
 XX AC ACA71029;
 XX DT 02-AUG-2003 (first entry)
 XX DE Human secreted/transmembrane protein (PRO) cDNA #50.
 XX KW Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
 XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 XX KW tissue typing.
 XX OS Homo sapiens.
 XX PN US2003032112-A1.
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PD 13-FEB-2003.
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Best Local Similarity 99.6%; Pred. No. 3.2e-241;
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DB 22 ATGAATGGCTTTGCTTCATCCTTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTTCACAGAGCCCAAGAGAGATGATGGTGAAGAGAGATCCAGAGAA 180
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QY 241 GATATGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTCACAAA 300
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DT 05-AUG-2003 (first entry)
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DE Human secreted polypeptide PRO702-encoding cDNA, SEQ ID NO:99.
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XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnary; gene therapy; gene; ss.
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Query Match 99.4%; Score 826.2; DB 7; Length 1016;

Best Local Similarity 99.6%; Pred. No. 3.2e-241; Mismatches 3; Indels 0; Gaps 0;
Matches 828; Conservative 0;

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DB 22 ATGAATGGCTTTTGCATCTCTTTCGGAAGAAACCAATTTATCTCTCTGGTACTATTCTT 81
QY 61 TTGCAATTCAGACTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 120
DB 82 TTGCAATTCAGACTCTGGGTCTGGATATTGATAGCCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACATTTTCACAGGACCCCAAGAGAGATGATGTTGCAAAAAGAGATCCAGAGAA 180
DB 142 ACACACACATTTTCACAGGACCCCAAGAGAGATGATGTTGCAAAAAGAGATCCAGAGAA 201
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DB 202 GAGGAAAGCATGGCAAGTGGGACCGCATGGGCGGAAAGCAATTAAGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 300
DB 262 GATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGGTGCACAA 321
QY 301 GGGGAAAAAGGTTTGGTTGGAAATACCTGGAGAAAAAGCAAGCAGGACTGTCTGTGAT 360
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QY 361 TGTGAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCGGCTCAAGACA 420
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 XX AC ACC89399;
 DT 11-AUG-2003 (first entry)
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 XX Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy; gene; ss.
 XX Homo sapiens.
 XX OS
 XX US2003027264-A1.
 XX PD
 XX 06-FEB-2003.
 XX PF
 XX 18-JUN-2002; 2002US-00174579.
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 Best Local Similarity 99.6%; Pred. No. 3.2e-241;
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 DB 82 TTGCAATTCAGAGTCGTGGGTCTCGATATTGATAGCCGTCTCTACCGCTGAAGTCGTGCC 141

QY 121 ACACACACATTTTCACAGGACCCCAAGAGGATGATGTTGAAAGAGGATCCAGGAGAA 180
 DB 142 ACACACACATTTTCACAGGACCCCAAGAGGATGATGTTGAAAGAGGATCCAGGAGAA 201

QY 181 GAGGAAAGCATGCCAAAGTGGGACGATGGGCGGCAAGAGAAATTAAGAGAACTGGGT 240
 DB 202 GAGGAAAGCATGCCAAAGTGGGACGATGGGCGGCAAGAGAAATTAAGAGAACTGGGT 261

QY 241 GATATGGGAGATCGGCAATTTTGGCAAGACTGGGCCCATTTGGAGAGAGGTGACAA 300
 DB 262 GATATGGGAGATCAGGCAATTTTGGCAAGACTGGGCCCATTTGGAGAGAGGTGACAA 321

QY 301 GGGGAAAAGGTTTGTCTTGGAAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTAT 360
 DB 322 GGGGAAAAGGTTTGTCTTGGAAATACCTGGAGAAAAGGCAAGCAGTACTGTCTGTAT 381

QY 361 TGTGGAACATACCGGAAATTTTGTGGCAACTGGATATTAGTATTTCCCGCTCAAGACA 420
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QY 601 AAGATGGCTCTTTTCGGGTTCATTGGCGTGAATGACCTTGAAGGAGGAGCAGTAC 660
 DB 622 AAGATGGCTCTTTTCGGGTTCATTGGCGTGAATGACCTTGAAGGAGGAGCAGTAC 681

QY 661 ATGTTTCACAGACACACTCCACTCAGAACTATAGCAACTGGAATGAGGGGAGACCAGC 720
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QY 721 GACCCCTATGTCATAGGACTGTGTGAGATGCTGTGAGCTCTGGCAGATGGAATGACACA 780
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AC ACA98190;
XX XX
DT 25-JUL-2003 (first entry)
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XX XX
KW Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; Gene; ss.
XX XX
OS Homo sapiens.
XX XX
PN US2003036144-A1.
XX XX
PD 20-FEB-2003.
XX XX
XX 01-JUL-2002; 2002US-00187601.
XX 18-SEP-1997; 97US-0059263P.
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Listing first 45 summaries

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SUMMARIES

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C 20	63	7.6	1200	4	US-09-134-000C-2614
C 21	62	7.5	1560	4	US-09-453-702B-264
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C 23	59.8	7.2	6674	4	US-09-620-312D-110
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C 25	59.6	7.2	1341	2	US-08-945-848-7
C 26	59.6	7.2	2363	2	US-08-945-848-6
C 27	58.8	7.1	2230	4	US-09-620-312D-282

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Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match 10.8%; Score 89.8; DB 1; Length 7218;

TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHEICAL: No. 6063901 relevant
ANTI-SENSE: No. 6063901 relevant
US-08-893-467A-1

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Matches 128; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 123 ACACACAAATTCACCAAGGACCCCAAGGAGATGATGTTGAAAAGGAGATCCAGGAGAGA 182
DB 780 ACTTACGGGTGACCAAGGAGGAGCAAGGAGCAACTGTGCTCCAGGACCTCCAGGAGAGA 839
QY 183 GGGAAAGCATGGCAAGTGGGAGCGATGGGCGGCAAGCAATTTAAAGGAGAACTGGGTGA 242
DB 840 GGGCAGCAAGGTGACATAGTCTACTGGCCCGGAGGGGGAACATGGCACCAGGGAGA 899
QY 243 TATGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGTTGACAAAGG 302
DB 900 CAAAGGGGACCTAGGCTTCCAGGAAACAAAGGGGACATGGGCATGAAGGGAGACAGGG 959
QY 303 GGAAGAAAGTTTGTCTTGGAAATACCTGGAGAAAAGGCAAGCAGTA 349
DB 960 GCCCATGGGGTCCCTGGAGCTCAGGAGGTAAAGTGTATGCTGAA 1006

RESULT 4

US-09-535-521-24
Sequence 24, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 24
LENGTH: 369
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(369)
US-09-535-521-24

Query Match
Best Local Similarity 7.7%; Score 64; DB 4; Length 369;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATTTCTACTACATCGTGCAGGAGAGAACTACAGGGAATCCCTTAACCCACTGCAG 530
DB 45 GAAGTCTACTACTTCGGCGAGAGCCCAAGAGTGGATCCAGGCCGGTTTGCCTGCAG 104
QY 531 GATTCGGGTGAATGCTAGCCATCCCAAGATGAAGTGCACACACTCATCGTGA 590
DB 105 CAAGTGCAGAGGGCGGCTGGCCGACATCCACAGCCCAAGAGGAGCAGGACTTCTGGCCAG 164
QY 591 CTATGTTGCCAAGAGTGGCTTTCTTTCGGGTGTTCTATGGCGTGAATGACCTTGAAGGGA 650

DB 165 GTATGCCAACAGAGGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 215
QY 651 GGGACAGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 216 GGGGGAGTTTATCTGGATGAGCAGAAACCCCT---GAACTATAGCAACTGGCGGCCGG 272
QY 711 GGAACCCAGCGACCCCTATGTTGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATG 770
DB 273 GGAGCCCAACACAGGGGGCCAGGGCGAGGACTGCTGATGATGAGGGCTCGGGGCGAGTG 332
QY 771 GAATGACACAGAGTGC 786
DB 333 GAATGACGCTTCTGC 348

RESULT 5

US-09-535-521-26/c
Sequence 26, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 26
LENGTH: 369
TYPE: DNA
ORGANISM: Canis familiaris
US-09-535-521-26

Query Match
Best Local Similarity 7.7%; Score 64; DB 4; Length 369;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATTTCTACTACATCGTGCAGGAGAGAACTACAGGGAATCCCTTAACCCACTGCAG 530
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QY 531 GATTCGGGTGAATGCTAGCCATCCCAAGATGAAGCTGCCAACACACTCATCGTGA 590
DB 265 CAAGTGCAGAGGGCGGCTGGCCAGCATCCACAGCCAAAGAGGAGCAGGACTTCTGGCCAG 206
QY 591 CTATGTTGCCAAGAGTGGCTTTCTTTCGGGTGTTCTATGGCGTGAATGACCTTGAAGGGA 650
DB 205 GTATGCCAACAGAGGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 155
QY 651 GGGACAGTACATGTTTCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 154 GGGGGAGTTTATCTGGATGAGCAGAAACCCCT---GAACTATAGCAACTGGCGGCCGG 98
QY 711 GGAACCCAGCGACCCCTATGTTGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATG 770
DB 97 GGAGCCCAACACAGGGGGCCAGGGCGAGGACTGCTGATGATGAGGGCTCGGGGCGAGTG 38
QY 771 GAATGACACAGAGTGC 786
DB 37 GAATGACGCTTCTGC 22

RESULT 6

US-09-535-521-7
Sequence 7, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.

;; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
;; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
;; FILE REFERENCE: AL-5
;; CURRENT APPLICATION NUMBER: US/09/535,521
;; CURRENT FILING DATE: 2000-03-24
;; EARLIER APPLICATION NUMBER: 60/125,913
;; EARLIER FILING DATE: 1999-03-24
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 7
;; LENGTH: 384
;; TYPE: DNA
;; ORGANISM: Canis familiaris
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(384)
US-09-535-521-7

Query Match 7.7%; Score 64; DB 4; Length 384;
Best Local Similarity 55.1%; Pred. No. 1.9e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATTTCTACTACATCGTCGAGAGAGAACTACAGGGAAATCCCTAACCCACTGCAG 530
DB 36 GAAGTGTCTACTACTTTCGCGGAGGAGCCCAAGATGGATCCAGGCCCGGTTTGCCTGCAG 95
QY 531 GATTGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGTGCACACACTCATCGCTGA 590
DB 96 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCCCAAGAGGAGGAGACTTCTTGGCCAG 155
QY 591 CTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCTATTTGGCGTGAATGACCTTGAAGGGA 650
DB 156 GTATGCCCAACAAGAGGCGACC-----TGGATTGGCCCTCGGGACCTGGACAGAGA 206
QY 651 GGGACACTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 207 GGGGGAGTTTATCTGGATGGAGCAAGAACCCCT---GAACTATAGCAACTGGCGGCCGG 263
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 264 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGATGCGAGGGCTCGGGGCACTG 323
QY 771 GAATGACACAGAGTGC 786
DB 324 GAATGACGCTTCTGC 339

RESULT 7
US-09-535-521-9/c
; Sequence 9, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-9

Query Match 7.7%; Score 64; DB 4; Length 384;
Best Local Similarity 55.1%; Pred. No. 1.9e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATTTCTACTACATCGTCGAGAGAGAACTACAGGGAAATCCCTAACCCACTGCAG 530
DB 349 GAAGTGTCTACTACTTTCGCGGAGGAGCCCAAGATGGATCCAGGCCCGGTTTGCCTGCAG 290
QY 531 GATTGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGTGCACACACTCATCGCTGA 590
DB 289 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCCCAAGAGGAGGAGGACTTCTTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCTATTTGGCGTGAATGACCTTGAAGGGA 650
DB 229 GTATGCCCAACAAGAGGCGACC-----TGGATTGGCCCTCGGGACCTGGACAGAGA 179
QY 651 GGGACACTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 178 GGGGGAGTTTATCTGGATGGAGCAAGAACCCCT---GAACTATAGCAACTGGCGGCCCG 122
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 121 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGATGCGAGGGCTCGGGGCACTG 62
QY 771 GAATGACACAGAGTGC 786
DB 61 GAATGACGCTTCTGC 46

RESULT 8
US-09-535-521-10
; Sequence 10, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(417)
US-09-535-521-10

Query Match 7.7%; Score 64; DB 4; Length 417;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATTTCTACTACATCGTCGAGAGAGAACTACAGGGAAATCCCTAACCCACTGCAG 530
DB 69 GAAGTGTCTACTACTTTCGCGGAGGAGCCCAAGATGGATCCAGGCCCGGTTTGCCTGCAG 128
QY 531 GATTGGGGTGGAAATGCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGA 590
DB 129 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCCCAAGAGGAGGAGGACTTCTTGGCCAG 188
QY 591 CTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCTATTTGGCGTGAATGACCTTGAAGGGA 650
DB 189 GTATGCCCAACAAGAGGCGACC-----TGGATTGGCCCTCGGGACCTGGACAGAGA 239
QY 651 GGGACACTACATGTTTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 240 GGGGGAGTTTATCTGGATGGAGCAAGAACCCCT---GAACTATAGCAACTGGCGGCCCG 296
QY 711 GGAACCCAGGACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTTGGCAGATG 770
DB 297 GGAGCCCAACAAGGGGGCCAGGGCGAGGAGTGGGTGATGATGCGAGGGCTCGGGGCACTG 356

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QY 771 GAATGACACAGAGTGC 786
Db 357 GAATGACGCTTCTGCG 372

RESULT 9
US-09-535-521-12/c
; Sequence 12, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-535-521-12

Query Match 7.7%; Score 64; DB 4; Length 417;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAG 530
Db 349 GAAGTGTCTACTACTTCGGCGAGAGCCCAAGAGTGGATCCAGGCGCGGTTTGCCTGCAG 290
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 289 CAAGCTGCAAGGGCGCTGGCAGATCCACAGCAAGAGAGGAGACTTCCTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
Db 229 GTATGCCAACAGAGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 179
QY 651 GGCACAGTACATGTTACAGACAACTCCACTGCAGAACTATAGCACTGGAATGAGGG 710
Db 178 GGGGAGTTTATCTGGATGGAGAGAACCCCT---GAACTATAGCAACTGGCGGCCGG 122
QY 711 GGAACCCAGCGACCCCTATGTTGTCATGAGGAGTGTGTGAGATGCTGAGCTCTGGCAGATG 770
Db 121 GGAAGCCCAACAGGGGGCCAGGGCGAGGACTGCTGATGATGAGGGCTCGGGGCAATG 62
QY 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGCG 46

RESULT 10
US-09-535-521-13
; Sequence 13, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 13
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(423)
US-09-535-521-13

Query Match 7.7%; Score 64; DB 4; Length 423;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAG 530
Db 75 GAAGTGTCTACTACTTCGGCGAGAGCCCAAGAGTGGATCCAGGCGCGGTTTGCCTGCAG 134
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 135 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGAGGAGACTTCCTGGCCAG 194
QY 591 CTATGTTGCCAAGAGTGGCTTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
Db 195 GTATGCCAACAGAGGGCACC-----TGGATTGGCTCCGGGACCTGGACAGAGA 245
QY 651 GGCACAGTACATGTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 246 GGGGAGTTTATCTGGATGGAGAGAACCCCT---GAACTATAGCAACTGGCGGCCGG 302
QY 711 GGAACCCAGCGACCCCTATGTTGTCATGAGGAGTGTGTGAGATGCTGAGCTCTGCAGATG 770
Db 303 GGAGGCCCAACAGGGGGCCAGGGCGAGGACTGCGTGATGATGAGGGGCTCGGGGCAATG 362
QY 771 GAATGACACAGAGTGC 786
Db 363 GAATGACGCTTCTGCG 378

RESULT 11
US-09-535-521-15/c
; Sequence 15, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-535-521-15

Query Match 7.7%; Score 64; DB 4; Length 423;
Best Local Similarity 55.1%; Pred. No. 2e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTTACTACATCGTCGAGGAGAGAGAACTACAGGAAATCCCTAACCCACTGCAG 530
Db 349 GAAGTGTCTACTACTTCGGCGAGAGCCCAAGAGTGGATCCAGGCGCGGTTTGCCTGCAG 290
QY 531 GATTGGGGTGAATGCTAGCCATGCCCAAGAGTGAAGCTGCCAACAACACTCATTCGCTGA 590
Db 289 CAAGCTGCAAGGGCGGCTGGCCAGCATCCACAGCAAGAGAGGAGACTTCCTGGCCAG 230
QY 591 CTATGTTGCCAAGAGTGGCTTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAGGGA 650
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Db 229 GTATGCCAACAGAGGGCACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 179
Qy 651 GGGACAGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 178 GGGGGAGTTTATCTGATGCAGAGAACCCCT---GAATATAGCAACTGGCGCCCGG 122
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGGAGCTGTGGAGATGCTGAGCTTGGCAGATG 770
Db 121 GGAGCCCAACACGGGGCCAGGGCGAGGACTGCGTGATGATGCAGGGCTCGGGGCAGTG 62
Qy 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGC 46

RESULT 12

US-09-535-521-16
; Sequence 16, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(561)
US-09-535-521-16

Query Match 7.7%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 2.4e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 471 GAAATTTCTACTACATCGTCGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
Db 213 GAAATGCTACTACTTCGCGAGAGGCCAACGAAGTGGATCCAGGCCCGGTTTGGCTGCAG 272
Qy 531 GATTCCGGGTGGAATCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGA 590
Db 273 CAAAGTGCAGAGGGCGGTGCCAGCATCCACAGCCAGAGAGAGGACTTCTTGGCCAG 332
Qy 591 CTATGTTGCCAAGAGTGGTCTTTTCGGGTGTTCAATTCGGCGTGAATGACCTTGAAGGGA 650
Db 333 GTATGCCAACAGAGGGCACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 383
Qy 651 GGGACAGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 384 GGGGGAGTTTATCTGATGACAGAACCCCT---GAATATAGCAACTGGCGCCCGG 440
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGGAGCTGTGGAGATGCTGAGCTTGGCAGATG 770
Db 441 GGAGCCCAACACGGGGCCAGGGCGAGGACTGCGTGATGATGCAGGGCTCGGGGCAGTG 500
Qy 771 GAATGACACAGAGTGC 786
Db 501 GAATGACGCTTCTGC 516

RESULT 13

US-09-535-521-18/c
; Sequence 18, Application US/09535521

; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-18

Query Match 7.7%; Score 64; DB 4; Length 561;
Best Local Similarity 55.1%; Pred. No. 2.4e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;
Qy 471 GAAATTTCTACTACATCGTCGAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
Db 349 GAAATGCTACTACTTCGCGAGAGGCCAACGAAGTGGATCCAGGCCCGGTTTGGCTGCAG 290
Qy 531 GATTCCGGGTGGAATCTAGCCATGCCCAAGGATGAAGTGCACACACTCATCGCTGA 590
Db 289 CAAAGTGCAGAGGGCGGTGCCAGCATCCACAGCCAGAGAGAGGACTTCTTGGCCAG 230
Qy 591 CTATGTTGCCAAGAGTGGTCTTTTCGGGTGTTCAATTCGGCGTGAATGACCTTGAAGGGA 650
Db 229 GTATGCCAACAGAGGGCACC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 179
Qy 651 GGGACAGTACATGTTCCACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
Db 178 GGGGGAGTTTATCTGATGACAGAACCCCT---GAATATAGCAACTGGCGCCCGG 122
Qy 711 GGAACCCAGGACCCCTATGGTCATGAGGAGCTGTGGAGATGCTGAGCTTGGCAGATG 770
Db 121 GGAGCCCAACACGGGGCCAGGGCGAGGACTGCGTGATGATGCAGGGCTCGGGGCAGTG 62
Qy 771 GAATGACACAGAGTGC 786
Db 61 GAATGACGCTTCTGC 46

RESULT 14

US-09-535-521-19
; Sequence 19, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(624)
US-09-535-521-19

Query Match 7.7%; Score 64; DB 4; Length 624;
Best Local Similarity 55.1%; Pred. No. 2.6e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTACTACATGCTGACAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
DB 276 GAAGTGCTACTACTTCGGCGAGAGGCCCAAGAGTGGATCCAGGCCCGGTTTGCTGCAG 335

QY 531 GATTGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGA 590
DB 336 CAAGCTGCAGGGCGGCTGGCAGCATCCACAGCCAGAGGAGGAGGACTTCCTGGCCAG 395

QY 591 CTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCATTTGGCGTGAATGACCTTTGAAAGGGA 650
DB 396 GTATGCCAACAGAGAGGACCC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 446

QY 651 GGCACAGTACATGTTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 447 GGGGAGTTTATCTCGATGAGAGNACCCCT---GAACTATAGCAACTGGCGGCCGG 503

QY 711 GGAACCCAGGACCCCTATGTCATGAGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 770
DB 504 GGAGCCCAACAACGGGGGCCAGGGCGAGGACTGCGTGATGATGCAGGGCTCGGGGCAGTG 563

QY 771 GAATGACACAGAGTGC 786
DB 564 GAATGAGCGCTTCTGC 579

RESULT 15
US-09-535-521-21/c
; Sequence 21, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: AL-5
; CURRENT APPLICATION NUMBER: US/09/535,521
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/125,913
; EARLIER FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-535-521-21

Query Match 7.7%; Score 64; DB 4; Length 624;
Best Local Similarity 55.1%; Pred. No. 2.6e-10;
Matches 174; Conservative 0; Mismatches 130; Indels 12; Gaps 2;

QY 471 GAAATCTACTACATGCTGACAGAGAGAACTACAGGGAATCCCTAACCCACTGCAG 530
DB 349 GAAGTGCTACTACTTCGGCGAGAGGCCCAAGAGTGGATCCAGGCCCGGTTTGCTGCAG 290

QY 531 GATTGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGA 590
DB 289 CAAGCTGCAGGGCGGCTGGCCAGCATCCACAGCCAGAGGAGGAGGACTTCCTGGCCAG 230

QY 591 CTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTCATTTGGCGTGAATGACCTTTGAAAGGGA 650
DB 229 GTATGCCAACAGAGAGGACCC-----TGGATTGGCCCTCCGGGACCTGGACAGAGA 179

QY 651 GGCACAGTACATGTTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGG 710
DB 178 GGGGAGTTTATCTCGATGAGAGNACCCCT---GAACTATAGCAACTGGCGGCCCGG 122

QY 711 GGAACCCAGGACCCCTATGTCATGAGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATG 770

Db 121 GGAGCCCAACACAGGGGGCCAGGGCGAGGACTGCGTGATGATGCAGGGCTCGGGGCAGTG 62
QY 771 GAATGACACAGAGTGC 786
Db 61 GAATGAGCGCTTCTGC 46

Search completed: March 11, 2004, 18:44:27
Job time : 95 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:50:29 ; Search time 362 Seconds

(without alignments)

8451.403 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatggcttgatcctt.....agttcatcaagaagaaaag 831

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
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16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	826.2	99.4	1016	9	US-09-978-697-96
3	826.2	99.4	1016	9	US-09-978-192A-96
4	826.2	99.4	1016	9	US-09-999-832A-96
5	826.2	99.4	1016	10	US-09-978-189-96
6	826.2	99.4	1016	10	US-09-978-608A-96
7	826.2	99.4	1016	10	US-09-978-585A-96
8	826.2	99.4	1016	10	US-09-978-191A-96
9	826.2	99.4	1016	10	US-09-978-403A-96
10	826.2	99.4	1016	10	US-09-978-564A-96
11	826.2	99.4	1016	10	US-09-981-833A-96
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13	826.2	99.4	1016	10	US-09-918-585A-96
14	826.2	99.4	1016	10	US-09-978-423A-96
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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      99.4%; Score 826.2; DB 9; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      22  ATGAATGGCTTTGGCATCCTTCTCGAAGAAACCAATTTATCTCTCTGGTACTATTTCCTT 81
QY      61  TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
DB      82  TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY     121  ACACACACAAATTCACAGGACCCCAAGAGATGATGTTGAAAGAGAGATCCAGAGAA 180
DB     142  ACACACACAAATTCACAGGACCCCAAGAGATGATGTTGAAAGAGAGATCCAGAGAA 201
QY     181  GAGGAAAGATCGGCAAAAGTGGGAGCGCATGCGGGCGGAAAGAAATTAAGGAGAACTGGGT 240
DB     202  GAGGAAAGATCGGCAAAAGTGGGAGCGCATGCGGGCGGAAAGAAATTAAGGAGAACTGGGT 261
QY     241  GATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGAGGTGACAA 300
DB     262  GATATGGGAGATCGGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGAGGTGACAA 321
QY     301  GGGGAAAGAGTTTCTTTGGAAATCTCTGAGAAAGCAAGCAGATCTGTCTGTGAT 360
DB     322  GGGGAAAGAGTTTCTTTGGAAATCTCTGAGAAAGCAAGCAGATCTGTCTGTGAT 381
QY     361  TTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTTGCCCGGCTCAAGACA 420
DB     382  TTGGAAGATACCGGAAATTTGTTGGCAACTGGATATTAGTATTTGCCCGGCTCAAGACA 441
QY     421  TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAACTGGAAGAAATTTCTAC 480
DB     442  TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGAACTGGAAGAAATTTCTAC 501
QY     481  TACATCGTGCAGGAGAGAAGAACTTACAGGAAATCCCTAACCCACTGCAGGATTCGGGGT 540
DB     502  TACATCGTGCAGGAGAGAAGAACTTACAGGAAATCCCTAACCCACTGCAGGATTCGGGGT 561
QY     541  GGAATGTAGCCATGCCCAAGATGAGCTGCCAACAATCTCATCTGCTGATGTGCC 600
DB     562  GGAATGTAGCCATGCCCAAGATGAGCTGCCAACAATCTCATCTGCTGATGTGCC 621
QY     601  AAGAGTGGCTTTCTTTGGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGAGACAGTAC 660
DB     622  AAGAGTGGCTTTCTTTGGGGTGTTCATTTGGCGTGAATGACCTTGAAGGGAGGAGACAGTAC 681
QY     661  ATGTTTCAGACACACATCCCACTGCAAGACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
DB     682  ATGTTTCAGACACACATCCCACTGCAAGACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
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RESULT 2

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US-09-978-697-96
; Sequence 96, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
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Query Match 99.4%; Score 826.2; DB 9; Length 1016;
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QY 1 ATGAATGGCTTTGGCATCTCTGTTTGGAGAAACCAATTATCTCTCTGGTACTATTCTTT 60
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 Db 322 GGGGAAAAAGTTTGTGGAATACCTGGAGAAAGCAAGCAGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATACCGGAAATTTGTTGGCACTGGGCACTGGATATTAGTATTTGCCGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAAATTTGTTGGCACTGGGCACTGGATATTAGTATTTGCCGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGAAATGTAGCAGGATAGGGAATAGGGAATAGGGAATTTCTAC 480
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 QY 481 TACATCGTCAGAGAGAGAGAGACTACAGGGAATCCCTAACCCACTGCGAGATTCGGGT 540
 Db 502 TACATCGTCAGAGAGAGAGAGACTACAGGGAATCCCTAACCCACTGCGAGATTCGGGT 561
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 Db 802 GAGTGCACTTTACCATGTACTTTCTGTGAGTTCATCAAGAGAAAG 852

RESULT 3
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 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C9
 CURRENT APPLICATION NUMBER: US/09/978,192A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
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Query Match 99.4%; Score 826.2; DB 9; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGAATGGCTTTGTCATCCTTCTCGAAGAAACCAATTTATCTCTCGTGGTACTATTTCTT	60
DB	22	ATGAATGGCTTTGTCATCCTTCTCGAAGAAACCAATTTATCTCTCGTGGTACTATTTCTT	81
QY	61	TTGCAAAATCAGAGTCGGTCTGGATATTGATAGCGTCTTACCGCTGAAGTCTGTGCC	120
DB	82	TTGCAAAATCAGAGTCGGTCTGGATATTGATAGCGTCTTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACACAATTTACACAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGGAGAA	180
DB	142	ACACACACAATTTACACAGGACCCAAAGGAGATGATGTTGAAAAGGAGATCCAGGAGAA	201
QY	181	GAGGAAAAGCATGGCAAGTGGAGCGCATGGGGCCGAAAGGAAATTAAGGAGACTGGGT	240
DB	202	GAGGAAAAGCATGGCAAGTGGAGCGCATGGGGCCGAAAGGAAATTAAGGAGACTGGGT	261
QY	241	GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAAGAGGGTGA	300
DB	262	GATATGGGAGATCAGGGCAATATTGGCAGACTGGGCCCATTTGGGAAAGAGGGTGA	321
QY	301	GGGGAAGAGTTCCTTTGGAATACCTTGGAGAAAAGGCAAGCAGGTACTGTCTGTAT	360
DB	322	GGGGAAGAGTTCCTTTGGAATACCTTGGAGAAAAGGCAAGCAGGTACTGTCTGTAT	381
QY	361	TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA	420
DB	382	TGTGGAAGATACCGGAATTTGTTGGCAACTGGATATTAGTATTGCCCGCTCAAGACA	441
QY	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAATTTAC	480
DB	442	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTTAGGGAACCTGAAGAGAAATTTAC	501
QY	481	TACATCGTGCAGGAAGAGAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT	540

Db 502 TACATGTCGAGAGAGAGAACTACAGGGATCCCTAACCCCACTGCAGGATCGGGGT 561
QY 541 GGAATGCTAGCCATGCCAAGGATGAAGTGCACACACTCATGCTGACTATGTTGCC 600
Db 562 GGAATGCTAGCCATGCCAAGGATGAAGTGCACACACTCATGCTGACTATGTTGCC 621
QY 601 AAGAGTGGCTTCTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGGACAGTAC 660
Db 622 AAGAGTGGCTTCTTTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGGACAGTAC 681
QY 661 ATGTTACACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
Db 682 ATGTTACACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
QY 721 GACCCCTATGTCATGAGAGCTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGAGCTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 801
QY 781 GAGTGCCTATTTACCATGTACTTTCTGCTGTGAGTTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCCTATTTACCATGTACTTTCTGCTGTGAGTTTCATCAAGAGAAAAAG 852

RESULT 4

US-09-999-832A-96
; Sequence 96, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
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Query Match 99.4%; Score 826.2; DB 9; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGCATCCTTGGCTTCGAAAGAAACCAATTTATCCTCTCTGTTACTATTCTT 60
DB 22 ATGAATGGCTTTGCATCCTTGGCTTCGAAAGAAACCAATTTATCCTCTCTGTTACTATTCTT 81

QY 61 TTGMAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTACCGCTGAGTCTGTGCC 120
DB 82 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGGTCTACCGCTGAGTCTGTGCC 141

QY 121 ACACACACAAATTTCCACGAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 180
DB 142 ACACACACAAATTTCCACGAGGACCCCAAGGAGATGATGTTGAAAAAGGAGATCCAGAGAA 201

QY 181 GAGGAAAGCATGGCAAGTGGGACCGCATGGGGCCGAAAGAAATTAAGGAGAACTCGGCT 240
DB 202 GAGGAAAGCATGGCAAGTGGGACCGCATGGGGCCGAAAGAAATTAAGGAGAACTCGGCT 261

QY 241 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGAGGTGACAA 300
DB 262 CATATGGGAGATCGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGAGGAGGTGACAA 321

QY 301 GGGGAAAAAGGTTTGTCTTGGAAATACCTGGGAGAAAGGCAAAAGCAGGACTGTCTGTGAT 360
DB 322 GGGGAAAAAGGTTTGTCTTGGAAATACCTGGGAGAAAGGCAAAAGCAGGACTGTCTGTGAT 381

QY 361 TGTGGAAGATACCGGAAATTTGTTGGCAACTGTGATATTAGTATTGCTCCGGCTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTGTTGGCAACTGTGATATTAGTATTGCTCCGGCTCAAGACA 441

QY 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCTGAAAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGATAGGGAATCTGAAAGAAATTTCTAC 501

QY 481 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGCT 540
DB 502 TACATCGTGCAGGAGAGAGAACTACAGGGAATCCCTACCCACTGCAGGATTCGGGCT 561

QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACTCATCTGCTGATGTGCT 600
DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACTCATCTGCTGATGTGCT 621

QY 601 AAGAGTGGCTTCTTTCGGGTGTTTCAATTGGGTGATGACCTTGAAGGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTTCGGGTGTTTCAATTGGGTGATGACCTTGAAGGGGAGGACAGTAC 681

QY 661 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
DB 682 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741

QY 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 780
DB 742 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGCTCTGCAGATGGAATGACACA 801

QY 781 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAAAAAG 831
DB 802 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCAAGAGAAAAAG 852

RESULT 5
US-09-978-189-96
; Sequence 96, Application US/09978189
; Publication No. US20030004102A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
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 ; APPLICANT: Shelton, David L.
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-259;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGAATGGCTTTGATCTCTTTCGAAGAAACCAATTTATCTCTCTGTAATTTCTT 60
 22 ATGAATGGCTTTGATCTCTTTCGAAGAAACCAATTTATCTCTCTGTAATTTCTT 81
 61 TTGCAAAATTCAGAGTCGGGTCTGGATATTTGATAGCCGTCCTACCGCTGAAGTCGTGCC 120
 82 TTGCAAAATTCAGAGTCGGGTCTGGATATTTGATAGCCGTCCTACCGCTGAAGTCGTGCC 141
 121 ACACACAAATTTCCACGAGACCAAGAGGATGATGGTGAAGAAAGGAGATCCAGGAGAA 180
 142 ACACACAAATTTCCACGAGACCAAGAGGATGATGGTGAAGAAAGGAGATCCAGGAGAA 201
 181 GAGGAAAGCATGCGCAAGTGGAGCGCATGGGCCCGAAAGGAATTAAGGAGAACTGGGT 240
 202 GAGGAAAGCATGCGCAAGTGGAGCGCATGGGCCCGAAAGGAATTAAGGAGAACTGGGT 261

QY 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAAGAGGTGACAAA 300
 DB 262 GATATGGAGATCAGGCAATATTTGGCAAGACTGGGCCATTTGGGAAAGAGGTGACAAA 321
 QY 301 GGGGAAAAGGTTTCTTGGAAATCTGGGAGAAAAGGCAAGGAGTACTGTCTGTGAT 360
 DB 322 GGGGAAAAGGTTTCTTGGAAATCTGGGAGAAAAGGCAAGGAGTACTGTCTGTGAT 381
 QY 361 TGTGAAGATACCGGAAATTTTGTGGCAACTGAGATATTAGTATTGCCCGGCTCAAGACA 420
 DB 382 TGTGAAGATACCGGAAATTTTGTGGCAACTGAGATATTAGTATTGCCCGGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAATCTGAAGAAATTTCTAC 480
 DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCAGGATAGGGAATCTGAAGAAATTTCTAC 501
 QY 481 TACATCGTGCAGGAGAGAACTTACAGGGAATCCCTAACCCCACTGCAGGATTCGGGGT 540
 DB 502 TACATCGTGCAGGAGAGAACTTACAGGGAATCCCTAACCCCACTGCAGGATTCGGGGT 561
 QY 541 GGAATGTAGCATGCCCAAGGATGAAGTCTGCCAACAACACTCATCTGCTGACTATGTGCC 600
 DB 562 GGAATGTAGCATGCCCAAGGATGAAGTCTGCCAACAACACTCATCTGCTGACTATGTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCGGGTGTTTCAATGGGCTGATGACCTTGAAGGAGGAGACAGTAC 660
 DB 622 AAGAGTGGCTTTCTTTCGGGTGTTTCAATGGGCTGATGACCTTGAAGGAGGAGACAGTAC 681
 QY 661 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
 DB 682 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
 QY 721 GACCCCTATGTCATGAGGATGTTGAGAGATGCTGAGCTCTGCGAGATGCAATGACACA 780
 DB 742 GACCCCTATGTCATGAGGATGTTGAGAGATGCTGAGCTCTGCGAGATGCAATGACACA 801
 QY 781 GAGTGCATCTTACCATGTACTTTTCTGTGAGTTCATCAAGAGAAAAAG 831
 DB 802 GAGTGCATCTTACCATGTACTTTTCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 6
 US-09-978-608A-96
 ; Sequence 96, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-96

Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 60
DB 22 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 180
DB 142 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 201
QY 181 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 261
QY 241 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 300
DB 262 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 321
QY 301 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 360
DB 322 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 381

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-96

Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 60
DB 22 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 180
DB 142 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 201
QY 181 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 261
QY 241 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 300
DB 262 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 321
QY 301 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 360
DB 322 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 381
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RESULT 7

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US-09-978-585A-96
; Sequence 96, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Kapier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 96
; LENGTH: 1016
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-96
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Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 60
DB 22 ATGAATGGCTTTCATCCTCTGCTCGAAGAAACCAATTTATCCTCTGCTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 180
DB 142 ACACACACAATTTCCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGTGAAGTCTGTGCC 201
QY 181 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 240
DB 202 GAGGAAAGCATGGCAAGTGGAGCGCATGGGCGCGAAGGAATTAAGAGGAACTCGGT 261
QY 241 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 300
DB 262 GATATGGGAGTCTGGGCAATATTGGCAAGTCTGGGCGCGAAGGAATTAAGAGGAACTCGGT 321
QY 301 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 360
DB 322 GGGGAAAAGGTTTCTTGGATACCTGGAGAAAAGGCAAGAGGAGTCTGTCTGTGAT 381
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QY 361 TGTGGAAGATACCGGAATTTGTTGCAACACTGGATATTAGTATTCGCCGGCTCAAGACA 420
Db 382 TGTGGAAGATACCGGAATTTGTTGCAACACTGGATATTAGTATTCGCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTCTCAAGATGATAGCAGGATTTAGGGAACCTGAGAGAAATTTCTAC 480
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QY 481 TACATCTGTCAGGAAGAGAACTACAGGAAATCCCTAACCCACTGACAGGATTCGGGGT 540
Db 502 TACATCTGTCAGGAAGAGAACTACAGGAAATCCCTAACCCACTGACAGGATTCGGGGT 561
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Db 562 GGAATGTCATGTCGCCAGGATGAAGCTGCAACACACTCATGCTGACTATGTTGCC 621
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Db 622 AAGAGTGGCTTCTTTCCGGGTGTTTCATTGGCGTGAATGACCTTTGAAAGGGAGGACAGTAC 681
QY 661 ATGTTACACACACACTCCACTGCGAGAACTATAGCAACTGGAATGAGGGGACCCGAC 720
Db 682 ATGTTACACACACACTCCACTGCGAGAACTATAGCAACTGGAATGAGGGGACCCGAC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCATCTTACCATGTTCTTTGCTGTGAGTTTCATCAAGAGAAAAAG 831
Db 802 GAGTGCATCTTACCATGTTCTTTGCTGTGAGTTTCATCAAGAGAAAAAG 852

RESULT 8
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; Sequence 96, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630F1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-05-13

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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: 60/085573
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTGATCCTCTTGCTTGAAGAAACCAATTTATCTCTGGTACTATTCTT 60
Db 22 ATGAATGGCTTTTGATCCTCTTGCTTGAAGAAACCAATTTATCTCTGGTACTATTCTT 81
QY 61 TTGMAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGTGAAGTCTGTGCC 120
Db 82 TTGCAATTCAGAGTCTGGGTCTGGATATTGATAGCGTCTCTACCGTGAAGTCTGTGCC 141
QY 121 ACACACACAAATTTCCACAGGACCCAAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 180
Db 142 ACACACACAAATTTCCACAGGACCCAAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 201
QY 181 GAGGAAAGCATGCGAAAGTGGGACCGCATCGGGCCGAAAGGAATTAAGAGAACTGGGT 240
Db 202 GAGGAAAGCATGCGAAAGTGGGACCGCATCGGGCCGAAAGGAATTAAGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGCAATATTGGCAACACTGGGCCCATTTGGGAAGAGGTGACAA 300
Db 262 GATATGGGAGATCAGGCAATATTGGCAACACTGGGCCCATTTGGGAAGAGGTGACAA 321
QY 301 GGGGAAAAAGGTTTGTGGAAATACCTGGGAAAAAGGCAAGCAGGTACTGTCTGTAT 360
Db 322 GGGGAAAAAGGTTTGTGGAAATACCTGGGAAAAAGGCAAGCAGGTACTGTCTGTAT 381
QY 361 TGTGAGAGTACCGGAAATTTGTGGCAACTGGATATTAGTATTCGCCGCTCAGACA 420
Db 382 TGTGAGAGTACCGGAAATTTGTGGCAACTGGATATTAGTATTCGCCGCTCAGACA 441
QY 421 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAGGGAACTGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGTCAAGAATGTGATAGCAGGATTAGGGAACTGAAGAGAAATTTCTAC 501
QY 481 TACATCGTCAGGAGAGAACTACAGGGATTCCTAACCCACTGCAGGATTCGGGT 540
Db 502 TACATCGTCAGGAGAGAACTACAGGGATTCCTAACCCACTGCAGGATTCGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCTGACTATGTTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAAACACACTCATCTGACTATGTTGCC 621
QY 601 AAGAGTGGCTTTCTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTCTTCGGGTGTTTCATTTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATCAGGGGAACCCAGC 720
Db 682 ATGTTTACAGACAACTCCACTGCAGAACTATAGCAACTGGAATCAGGGGAACCCAGC 741
QY 721 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801

QY 781 GAGTCCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAAAG 831
DB 802 GAGTCCATCTTACCATGTACTTTCTGTGTGAGTTTCATCAAGAGAAAAAG 852

RESULT 9

US-09-978-403A-96
; Sequence 96, Application US/09978403A
; Publication No. US2003050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/083322

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Db	142	ACACACAAATTTCCACAGGAGCCCAAAAGGAGATGATCGTGAAAAAGGAGATCCAGAGAA	201
Qy	181	GAGGAAAGCATGGCAAAGTGGGACGATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT	240
Db	202	GAGGAAAGCATGGCAAAGTGGGACGATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT	261
Qy	241	GATATGGGAGATCGGGGCAATATTGGCAAAGACTGGGCCCATTTGGGAAGAGGGGTGACAA	300
Db	262	GATATGGGAGATCAGGCGNATATTGGCAAAGCTGGGCCCATTTGGGAAGAGGGGTGACAA	321
Qy	301	GGGAAAAAGGTTTGCTTTGGAAATCCTGGAGAAAAAGGCAAAAGCAGGACTGTCTGTGAT	360
Db	322	GGGAAAAAGGTTTGCTTTGGAAATCCTGGAGAAAAAGGCAAAAGCAGGACTGTCTGTGAT	381
Qy	361	TGTGCAAGATACCCGGAATTTGTTGGCAACTGGATATTAGTATTCGCCGGCTCAAGACA	420
Db	382	TGTGCAAGATACCCGGAATTTGTTGGCAACTGGATATTAGTATTCGCCCTCAAGACA	441
Qy	421	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC	480
Db	442	TCTATGAAGTTTGTCAAGATGTGATAGCAGGATTAGGGAATCTGAAGAGAAATTTCTAC	501
Qy	481	TACATCGTCGAGGAGAGAGAACTACAGGGAATCCCTTACCACACTGCAGGAATTCGGGT	540
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Qy	541	GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACTCATCTGACTATGTTGCC	600
Db	562	GGAATGTAGCCATGCCCAAGGATGAAGCTGCCAACACTCATCTGACTATGTTGCC	621
Qy	601	AAGAGTGCTCTTTTCGGGTGTTCAATTTGGCGTGTAATGACCTTGAAAGGGAGGACAGTAC	660
Db	622	AAGAGTGCTCTTTTCGGGTGTTCAATTTGGCGTGTAATGACCTTGAAAGGGAGGACAGTAC	681
Qy	661	ATGTTTCAGACAACACTCCACTGCAGAACTATAGCAACTGGGAATGAGGGGAAACCCAGC	720
Db	682	ATGTTTCAGACAACACTCCACTGCAGAACTATAGCAACTGGGAATGAGGGGAAACCCAGC	741
Qy	721	GACCCCTATGTCATGAGGACTGTGTGGAGATCCTGAGCTCTGGCAGATGGAATGACACA	780
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Qy	781	GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAAAG	831
Db	802	GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAAAAAG	852

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RESULT 10
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US-Sequence 96, Application US/09978564A
/ Publication NO. US20030050241A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Descovets, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Grittisen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Klayvin, Ivar J.

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Query Match	99.4%	Score 826.2	DB 10	Length 1016
Best Local Similarity	99.6%	Pred. No. 5,7e-258		
Matches 828	Conservative	0	Mismatches 3	Indels 0
Gaps	0			
QY	1	ATGAATGCTTTGATCTCTGCTTCGAAGAACCAATTATCTCTCTGGTACTATTTCTT	60	
Db	22	ATGAATGCTTTGATCTCTGCTTCGAAGAACCAATTATCTCTCTGGTACTATTTCTT	81	
QY	61	TTGCAAAATTCAGAGTCTGGGCTGGATATTGATAGCGCTCTACCGCTGAAGCTGTGTC	120	

APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acetated and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;

Best Local Similarity 99.6%; Pred. No. 5.7e-258; Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTGTCATCCCTTGGTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 60
 DB 22 ATGAATGGCTTTGTCATCCCTTGGTTCGAAGAACCAATTTATCTCTCTGCTACTATTTCTT 81
 QY 61 TTGCAAAATTCAGAGTCTGGTCTGATATTGATAGCCCTCTACCGCTGAAGTCTGTGCC 120
 DB 82 TTGCAAAATTCAGAGTCTGGTCTGATATTGATAGCCCTCTACCGCTGAAGTCTGTGCC 141
 QY 121 ACACACACAATTTCCACGAGACCCAAAGAGATGATGTTGAAAGAGATCCAGAGAA 180
 DB 142 ACACACACAATTTCCACGAGACCCAAAGAGATGATGTTGAAAGAGATCCAGAGAA 201
 QY 181 GAGGGAAGATCGGCAAGTGGAGCGCATGGGGCCGAAAGGAATTAAGAGGAATCTGGT 240
 DB 202 GAGGGAAGATCGGCAAGTGGAGCGCATGGGGCCGAAAGGAATTAAGAGGAATCTGGT 261
 QY 241 GATATGGAGATCGGGCAATATTCGCAAGCTGGCCCATTTGGGAAGAGGTGACAAA 300
 DB 262 GATATGGAGATCGGGCAATATTCGCAAGCTGGCCCATTTGGGAAGAGGTGACAAA 321
 QY 301 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAGCAAGCAGGTACTGTCTGTGAT 360
 DB 322 GGGGAAAAAGTTTGTCTGGAATACCTGGAGAAAAGCAAGCAGGTACTGTCTGTGAT 381
 QY 361 TGTGGAAGATCCGGAATTTGTTGGCAATCTGGATATTAGTATTCCTGGCTCAAGACA 420
 DB 382 TGTGGAAGATCCGGAATTTGTTGGCAATCTGGATATTAGTATTCCTGGCTCAAGACA 441
 QY 421 TCTATGAAGTTTGTCAAGAAATCTAGCAGGATTTAGGAAAAGTGAAGAGAAATTTCTAC 480
 DB 442 TCTATGAAGTTTGTCAAGAAATCTAGCAGGATTTAGGAAAAGTGAAGAGAAATTTCTAC 501
 QY 481 TACATCGTCAGAGAGAGAGAACTACAGGAAATCCCTAACCCCTCGCAGGATTCGGGT 540

DB 502 TACATCGTCAGAGAGAGAACTACAGGAATCCCTAACCCCTCGCAGGATTCGGGT 561
 QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACATCATCGTGTGACTATGTTGCC 600
 DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACATCATCGTGTGACTATGTTGCC 621
 QY 601 AAGAGTGGCTTTCTTTCGGGTGTTTATTTGGCTGTAATGACCTTTGAAAGGGGACAGTAC 660
 DB 622 AAGAGTGGCTTTCTTTCGGGTGTTTATTTGGCTGTAATGACCTTTGAAAGGGGACAGTAC 681
 QY 661 ATGTTTCACAGACACATCCCACTGAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
 DB 682 ATGTTTCACAGACACATCCCACTGAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
 QY 721 GACCCCTATGTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 DB 742 GACCCCTATGTCATGAGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 QY 781 GAGTGGCACTTTACCATGCTACTTTGCTGTGAGTTCATCAAGAGAAAAAG 831
 DB 802 GAGTGGCACTTTACCATGCTACTTTGCTGTGAGTTCATCAAGAGAAAAAG 852

RESULT 11

; US-09-999-833A-96
 ; Sequence 96, Application US/09999833A
 ; Publication No. US20030054405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C65
 ; CURRENT APPLICATION NUMBER: US/09/999,833A
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/082564	PRIOR FILING DATE: 1998-04-21
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred. No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCTTTTCATCCCTTCTCGAAGAACCAATTTATCTCTCTGTAATTTCTT 60
Db 22 ATGAATGGCTTTTCATCCCTTCTCGAAGAACCAATTTATCTCTCTGTAATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
Db 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTACACAGAGCCCAAGAGATGATGTTGAAAAGAGAGATCCAGGAGAA 180
Db 142 ACACACAAATTTACACAGAGCCCAAGAGATGATGTTGAAAAGAGAGATCCAGGAGAA 201
QY 181 GAGGAAAGCATCGCAAGTGGGACCATGGGCGCAAGAGATTAAGAGGAGATCGGT 240
Db 202 GAGGAAAGCATCGCAAGTGGGACCATGGGCGCAAGAGATTAAGAGGAGATCGGT 261
QY 241 GATATGGAGATCGGCGCAATTTGCAAGACTGGGCCCATTTGGGAAGAGGTTGACAAA 300
Db 262 GATATGGAGATCGGCGCAATTTGCAAGACTGGGCCCATTTGGGAAGAGGTTGACAAA 321
QY 301 GGGGAAAGGTTTGTCTGGAATACCTGAGAAAGCAAGCAAGTACTGTCTGTGAT 360
Db 322 GGGGAAAGGTTTGTCTGGAATACCTGAGAAAGCAAGCAAGTACTGTCTGTGAT 381
QY 361 TGTGGAAGTACCGGAAATTTGTTGACAACTGATATTAGTATTGCCCCGGCTCAAGACA 420
Db 382 TGTGGAAGTACCGGAAATTTGTTGACAACTGATATTAGTATTGCTCGGCTCAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTAGTACAGAGGATAGGAACTGGAAGAGAAATTTCTAC 480
Db 442 TCTATGAAGTTTGTCAAGATGTAGTACAGAGGATAGGAACTGGAAGAGAAATTTCTAC 501
QY 481 TACATCGTGCAGAGAGAGAACTACAGGGAATCCCTAAACCCTGCAGGATTCGGGGT 540
Db 502 TACATCGTGCAGAGAGAGAACTACAGGGAATCCCTAAACCCTGCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGAGATGAGCTGCCAACAACATCGTACTGATTTGCC 600
Db 562 GGAATGCTAGCCATGCCCAAGAGATGAGCTGCCAACAACATCGTACTGATTTGCC 621
QY 601 AAGAGTGGCTTTCTCGGGTGTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 660
Db 622 AAGAGTGGCTTTCTCGGGTGTTCATTGGCGTGAATGACCTTGAAGGGAGGACAGTAC 681
QY 661 ATGTTCAACAGACAACACTCCATCGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 720
Db 682 ATGTTCAACAGACAACACTCCATCGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGC 741
QY 721 GACCCCTATGCTCATGAGCACTGTGTGGAGATGCTGAGCTCTGGCAGATGAATGACACA 780
Db 742 GACCCCTATGCTCATGAGCACTGTGTGGAGATGCTGAGCTCTGGCAGATGAATGACACA 801
QY 781 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAGAAAAAG 831
Db 802 GAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAGAGAAAAAG 852

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RESULT 12

US-09-981-915A-96
; Sequence 96, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5,7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATGAATGGCTTTCATCTCTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCCT	60
Db	22	ATGAATGGCTTTCATCTCTCTCGAAGAACCAATTTATCTCTCTGGTACTATTTCCT	81
QY	61	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	120
Db	82	TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC	141
QY	121	ACACACACAATTTCCACGAGACCCCAAGAGGATGATGTTGAAAAGGAGATCCAGAGAA	180
Db	142	ACACACACAATTTCCACGAGACCCCAAGAGGATGATGTTGAAAAGGAGATCCAGAGAA	201
QY	181	GAGGAAAAGCATGCGCAAGTGGGCGCATGGGGCGGCAAGAAATTAAGGAGAACTGGGT	240
Db	202	GAGGAAAAGCATGCGCAAGTGGGCGCATGGGGCGGCAAGAAATTAAGGAGAACTGGGT	261
QY	241	GATATGGGAGATCGGGGCAATATTGGCAGACTGGGCCCATTTGGGAGAGAGGCTGACAA	300

Db 262 CATATGGAGATCAGGCAATATGCAAGATCTGGCCCATTTGGGAAGAGGGTGCACAA 321
 Qy 301 GGGGAAAAAGTTTGTCTTGAATACCTCGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 360
 Db 322 GGGGAAAAAGTTTGTCTTGAATACCTCGAGAAAAGGCAAGCAGGTACTGTCTGTGAT 381
 Qy 361 TGTGGAAGATACCGGAATTTGTGGAACCTGGAATATGATATGATGATGATGATGATGAT 420
 Db 382 TGTGGAAGATACCGGAATTTGTGGAACCTGGAATATGATATGATGATGATGATGAT 441
 Qy 421 TCTATGAAGTTTCTCAAGATGTGATGAGCAGGATTTAGGGAACCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTCTCAAGATGTGATGAGCAGGATTTAGGGAACCTGAAGAGAAATTTCTAC 501
 Qy 481 TACATGTCGAGAGAGAGAACTACAGGGAATCCCTAAACCTGAGGATTCGGGGT 540
 Db 502 TACATGTCGAGAGAGAGAACTACAGGGAATCCCTAAACCTGAGGATTCGGGGT 561
 Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACTCATGCTGACTATGTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGCTGCAACACACTCATGCTGACTATGTTGCC 621
 Qy 601 AGAGTGGCTTTCTTGGGTGTTCAATGCGGTGAATGACCTTGAAGGGAGGGACAGTAC 660
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 Qy 661 ATGTTCCACAGACACACTCCCTGAGACTATAGCACTGATGAGGGAGGGAGCCAGC 720
 Db 682 ATGTTCCACAGACACACTCCCTGAGACTATAGCACTGATGAGGGAGGGAGCCAGC 741
 Qy 721 GACCCCTATGTCATGAGGACTGTGAGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGTCATGAGGACTGTGAGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 Qy 781 GAGTGCATCTTACCATGCTACTTCTGTGATGCTCATCAAGAGAAAAAG 831
 Db 802 GAGTGCATCTTACCATGCTACTTCTGTGATGCTCATCAAGAGAAAAAG 852

RESULT 13

US-09-978-824-96

; Sequence 96, Application US/09978824

; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC14
 ; CURRENT APPLICATION NUMBER: US/09/978,824
 ; CURRENT FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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99 PRIOR APPLICATION NUMBER: 60/085697
100 PRIOR FILING DATE: 1998-05-15

Query Match 99.4%; Score 826.2; DB 10; Length 1016;

Best Local Similarity 99.6%; Pred. No. 5.7e-258;

Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGCTTTGTCATCTCTGTCGAGAGAACCAATTTATCTCTGCTGCTACTTTCTTT 60
DB 22 ATGAATGCTTTGTCATCTCTGTCGAGAGAACCAATTTATCTCTGCTGCTACTTTCTTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTGATAGCGCTCTACCGCTGAAGTCTGTGCC 141
QY 121 ACACACAAATTTACACAGGACCCAAAGAGATGATGTCGAAAAGAGAGATCCAGAGAA 180
DB 142 ACACACAAATTTACACAGGACCCAAAGAGATGATGTCGAAAAGAGAGATCCAGAGAA 201
QY 181 GAGGAAAAGCATGCGAAGTGGGACCGCATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT 240
DB 202 GAGGAAAAGCATGCGAAGTGGGACCGCATGGGGCCGAAAGGAATTTAAAGGAGAACTGGGT 261
QY 241 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTTGGGAAGAGAGGTGACAA 300
DB 262 GATATGGGAGATCGGGGCAATATTGGCAAGACTGGGCCCAATTTGGGAAGAGAGGTGACAA 321
QY 301 GGGGAAAAGGTTTGTCTTGGAAATACCTGGGAAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 322 GGGGAAAAGGTTTGTCTTGGAAATACCTGGGAAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTTGTGGACAACTGGATATTAGTATTGCCCGGCTCAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTTGTGGACAACTGGATATTAGTATTGCCCGGCTCAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGGAATCTAGAGAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGATGTGATAGCGGATTTAGGGAATCTAGAGAGAAATTTCTAC 501
QY 481 TACATCGTCAGGAGAGAGAACTTACAGGAATTCCTTAACCCACTCCAGGATTCGGGGT 540
DB 502 TACATCGTCAGGAGAGAGAACTTACAGGAATTCCTTAACCCACTCCAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAGCTGCCAACACACTCATCGCTGACTATTGTGCC 600
DB 562 GGAATGCTAGCCATGCCCAAGGATGAGCTGCCAACACACTCATCGCTGACTATTGTGCC 621
QY 601 AAGAGTGGCTTCTTTTCGGGTGTTCATTGGCTGTAATGACCTTTGAAAAGGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTTTCGGGTGTTCATTGGCTGTAATGACCTTTGAAAAGGGAGGACAGTAC 681
QY 661 ATGTTCACAGACAACTCCACTGCAGAACTATTAGCACTGGAATGAGGGGGAACCCAGC 720

Db 682 ATGTCCACACACACACTCCCTCCAGACATATAGCACTGGAATGAGGGGAAACCCAGC 741
QY 721 GACCCCTATGCTATGAGAGCTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
Db 742 GACCCCTATGCTATGAGAGCTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGCCATCTTACCAGTACTTTGCTGTGAGTTTCATCAAGAGAAAAG 831
Db 802 GAGTGCACTTACCAGTACTTTGCTGTGAGTTTCATCAAGAGAAAAG 852

RESULT 14

US-09-918-585A-96
Sequence 96, Application US/09918585A
Publication No. US20030060406A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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67 PRIOR FILING DATE: 1998-05-15
68 PRIOR APPLICATION NUMBER: 60/086023

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
Best Local Similarity 99.6%; Pred No. 5.7e-258;
Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGCGTTTGGATCCTTCTGCTTGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 60
DB 22 ATGAATGCGTTTGGATCCTTCTGCTTGAAGAAACCAATTTATCTCTCTGCTACTATTTCTT 81
QY 61 TTGCAAAATTCAGAGTCTGGGTCTGGATATTCATAGCCGCTCTACCGCTGGAAGTCTGTGCC 120
DB 82 TTGCAAAATTCAGAGTCTGGGTCTGGATATTCATAGCCGCTCTACCGCTGGAAGTCTGTGCC 141
QY 121 ACACACAAATTTCCAGAGCCCAAGAGGATATGGTGAAGAGGAGATCCAGGAGAA 180
DB 142 ACACACAAATTTCCAGAGCCCAAGAGGATATGGTGAAGAGGAGATCCAGGAGAA 201
QY 181 GAGGAAAGCATGGCAAAAGTGGACCGCATGGGCGCAAAAGGAATTAAGAGGAGAACTGGGT 240
DB 202 GAGGAAAGCATGGCAAAAGTGGACCGCATGGGCGCAAAAGGAATTAAGAGGAGAACTGGGT 261
QY 241 GATATGGAGATCGGGGCAATTTTGGCAAGTCTGGGCCCATTTGGGAAGAGGATGACAAA 300
DB 262 GATATGGAGATCGGGGCAATTTTGGCAAGTCTGGGCCCATTTGGGAAGAGGATGACAAA 321
QY 301 GGGGAAAAAGTTTCTTGGATACCTCGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 360
DB 322 GGGGAAAAAGTTTCTTGGATACCTCGAGAAAAAGGCAAGCAGGTACTGTCTGTGAT 381
QY 361 TGTGGAAGATACCGGAAATTTTGTGGCAACTGGATATTTAGTATTTGCCCGGCTCAAGACA 420
DB 382 TGTGGAAGATACCGGAAATTTTGTGGCAACTGGATATTTAGTATTTGCCCGGCTCAAGACA 441
QY 421 TCTATGAAGTTTGTCAAGATGTGTAGCAGGATTTAGGGAACTGGAAGAAATTTCTAC 480
DB 442 TCTATGAAGTTTGTCAAGATGTGTAGCAGGATTTAGGGAACTGGAAGAAATTTCTAC 501
QY 481 TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCCTGCGAGGATTCGGGGT 540
DB 502 TACATCGTGCAGGAAGAGAACTACAGGGAATCCCTAACCCCTGCGAGGATTCGGGGT 561
QY 541 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATGTGCC 600
DB 562 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATGTGCC 621
QY 601 AAGAGTGGCTTCTTTTGGGTGTTTCACTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 660
DB 622 AAGAGTGGCTTCTTTTGGGTGTTTCACTGGCGTGAATGACCTTGAAGAGGAGGACAGTAC 681
QY 661 ATGTTCAAGACACACTCCACTGCAAGTATAGCACTGGAATGAGGGGGAACCCAGC 720
DB 682 ATGTTCAAGACACACTCCACTGCAAGTATAGCACTGGAATGAGGGGGAACCCAGC 741
QY 721 GACCCCTATGCTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
DB 742 GACCCCTATGCTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
QY 781 GAGTGGCAATCTTACCATGACTTTTGTGTGAGTTTCATCAAGAGAAAAAG 831
DB 802 GAGTGGCAATCTTACCATGACTTTTGTGTGAGTTTCATCAAGAGAAAAAG 852

RESULT 15
US-09-978-423A-96
; Sequence 96, Application US/0978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.

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APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918595
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/079663
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.4%; Score 826.2; DB 10; Length 1016;
 Best Local Similarity 99.6%; Pred. No. 5.7e-258;
 Matches 828; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 ATGAATGGCTTTCATCCCTTCTCGAAGAACCAATTTATCTCTCTGTACTATTTCTT 60
 Db 22 ATGAATGGCTTTCATCCCTTCTCGAAGAACCAATTTATCTCTCTGTACTATTTCTT 81
 Qy 61 TTGCAAAATTCAGAGTCTGGGCTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 120
 Db 82 TTGCAAAATTCAGAGTCTGGGCTCTGGATATTGATAGCCGCTCTACCGCTGAAGTCTGTGCC 141
 Qy 121 ACACACAAATTTCCAGACCCCAAGAGGATGATGGTGAAAGAGGAGATCCAGGAGAA 180
 Db 142 ACACACAAATTTCCAGACCCCAAGAGGATGATGGTGAAAGAGGAGATCCAGGAGAA 201
 Qy 181 GAGGGAAGCATGCGAAAGTGGGACCGCATGGGCGCGAAGGAATTAAGAGGAAGTGGGT 240
 Db 202 GAGGGAAGCATGCGAAAGTGGGACCGCATGGGCGCGAAGGAATTAAGAGGAAGTGGGT 261
 Qy 241 GATATGGGAGATCGGGCAATATTTGGCAAGATCTGGGCCCATTTGGGAAGAGGGTGACAAA 300
 Db 262 GATATGGGAGATCAGGGCAATATTTGGCAAGATCTGGGCCCATTTGGGAAGAGGGTGACAAA 321
 Qy 301 GGGGAAAAAGGTTTGTCTGGAATACCTGGGAAAAAGGCAAGGAGGAGTACTCTCTGTGAT 360
 Db 322 GGGGAAAAAGGTTTGTCTGGAATACCTGGGAAAAAGGCAAGGAGGAGTACTCTCTGTGAT 381
 Qy 361 TGTGGAAGATACCGGAAATTTGTTGCAACCTGGATATTAGTATTGCCCGGCTCAAGACA 420
 Db 382 TGTGGAAGATACCGGAAATTTGTTGCAACCTGGATATTAGTATTGCCCGGCTCAAGACA 441

Qy 421 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC 480
 Db 442 TCTATGAAGTTTGTCAAGAAATGTGATAGCAGGGATTTAGGGAACCTGAAGAGAAATTTCTAC 501
 Qy 481 TACATCGTGCAGGAAGAGAAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 540
 Db 502 TACATCGTGCAGGAAGAGAAACTACAGGGAATCCCTAACCCACTGCAGGATTCGGGGT 561
 Qy 541 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATTTGCC 600
 Db 562 GGAATGCTAGCCATGCCCAAGGATGAAGTGCACACACACTCATCGCTGACTATTTGCC 621
 Qy 601 AAGAGTGGCTTCTTTCCGGGTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 660
 Db 622 AAGAGTGGCTTCTTTCCGGGTTCATTGGCGTGAATGACCTTGAAGGAGGACAGTAC 681
 Qy 661 ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 720
 Db 682 ATGTTCAACAGAACCACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAAACCCAGC 741
 Qy 721 GACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 780
 Db 742 GACCCCTATGGTTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACA 801
 Qy 781 GAGTGGCACTTTACCATGTAATTTCTGTGTGAGTTTCATCAAGAGAAAAAG 831
 Db 802 GAGTGGCACTTTACCATGTAATTTCTGTGTGAGTTTCATCAAGAGAAAAAG 852

Search completed: March 11, 2004, 18:42:46
 Job time : 373 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 16:44:12 ; Search time 2531 seconds

(without alignments)
9804.612 Million cell updates/sec

Title: US-09-600-932-1_COPY_6_836

Perfect score: 831

Sequence: 1 atgaatggcttgcctcctt.....agttcatcaagaagaaaag 831

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsl1:*

29: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827.8	99.6	834	29	AY409410 Homo sapi
2	823	99.0	834	29	AY409411 Pan trogl
3	669.6	80.6	752	12	BM009998 603630745
4	644.4	77.5	4591	11	AK028423 Mus muscu

5	642.8	77.4	834	29	AY409412	AY409412 Mus muscu
6	462.8	55.7	560	13	EX494095	EX494095 DXFZP779A
7	455	54.8	955	10	BB612129	BB612129 BB612129
8	444.4	53.5	609	12	BM010788	BM010788 603629302
9	427.8	51.5	457	13	EX496500	EX496500 DXFZP779M
10	409.2	49.2	492	10	BF078010	BF078010 228226 MA
11	392.8	47.3	930	14	CF378429	CF378429 AGENCOURT
12	389.6	45.9	747	14	CB228545	CB228545 AGENCOURT
13	386	45.5	499	12	BI467460	BI467460 389071 MA
14	308.4	37.1	636	13	EX671934	EX671934 BX671934
15	302.6	36.4	654	12	BI067078	BI067078 P9f1n.pk0
16	297	35.7	890	14	CF378456	CF378456 AGENCOURT
17	274.8	33.1	380	10	BB869893	BB869893 BB869893
18	273.6	32.9	354	10	AW435866	AW435866 75149 MAR
19	268.6	32.3	1239	12	BM551435	BM551435 AGENCOURT
20	265.4	31.9	361	10	BB869996	BB869996 BB869996
21	255.2	30.7	325	13	BY332718	BY332718 BY332718
22	251	30.2	743	13	BU290748	BU290748 603608166
23	249	30.0	451	10	AW355638	AW355638 P9f1n.pk0
24	241.6	29.1	486	12	BM426695	BM426695 P9f1n.pk0
25	239.6	28.8	344	13	BY008444	BY008444 BY008444
26	239	28.8	1383	11	AK003121	AK003121 Mus muscu
27	238	28.6	326	14	R29493	R29493 F1-1006D 22
28	235.8	28.4	1201	13	EX427124	EX427124 EX427124
29	229	27.6	894	13	BU147034	BU147034 AGENCOURT
30	218.2	26.3	1143	13	EX333394	EX333394 EX333394
31	201	24.2	362	14	R97480	R97480 YG53H02.r1
32	197.4	23.8	670	14	CB141360	CB141360 K-EST0194
33	190.6	22.9	1132	13	EX394893	EX394893 EX394893
34	188.6	22.7	324	13	BY331120	BY331120 BY331120
35	184.6	22.2	1201	13	EX394625	EX394625 EX394625
36	184.4	22.2	1201	13	EX394624	EX394624 EX394624
37	180	21.7	734	14	CB430533	CB430533 606434 MA
38	179	21.5	962	13	BQ927000	BQ927000 AGENCOURT
39	174.2	21.0	505	14	CB418352	CB418352 591149 MA
40	172.6	20.8	962	13	BQ69775	BQ69775 AGENCOURT
41	172.4	20.7	893	10	BF314316	BF314316 601901046
42	169.4	20.4	610	14	CB056003	CB056003 NISC_jj11
43	162.8	19.6	569	29	CE798050	CE798050 tigr-gss-
44	161	19.4	590	9	AV690347	AV690347 AV690347
45	157.2	18.9	645	13	BU404074	BU404074 604136366

ALIGNMENTS

RESULT 1	AY409410	834 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	AY409410	Homo sapiens COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY409410	Genomic survey sequence.			
ACCESSION	AY409410.1	GI:39765378			
VERSION	AY409410.1	GI:39765378			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 834)			
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2	(bases 1 to 834)			
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..834

gene 1..834

ORIGIN

Query Match 99.6%; Score 827.8; DB 29; Length 834;

Best Local Similarity 99.8%; Pred. No. 18-217; Indels 0; Gaps 0;

Matches 829; Conservative 0; Mismatches 2;

Qy 1 ATGAATGGCTTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGTTACTATTTCTT 60

Db 1 ATGAATGGCTTTTCACCTCTGCTTTCGAAGAACCAATTTATCTCTCTGTTACTATTTCTT 60

Qy 61 TTGCAATTCAGAGTCTGGTCTGGATATGATAGCCCTTACCGCTGAAGTCTGTGCC 120

Db 61 TTGCAATTCAGAGTCTGGTCTGGATATGATAGCCCTTACCGCTGAAGTCTGTGCC 120

Qy 121 ACACACAAATTTTCCAGACCCCAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 180

Db 121 ACACACAAATTTTCCAGACCCCAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 180

Qy 181 GAGGAAAGCATGCGAAATGCGACCCATGCGGCGCAAGAGATTAAGAGAACTGGGT 240

Db 181 GAGGAAAGCATGCGAAATGCGACCCATGCGGCGCAAGAGATTAAGAGAACTGGGT 240

Qy 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGGGGTGACAA 300

Db 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGGGGTGACAA 300

Qy 301 GGGGAAAGAGTTTGGTGGAAATGATGAGGAAAGAGGCAAGAGGATCTGTCTGTGAT 360

Db 301 GGGGAAAGAGTTTGGTGGAAATGATGAGGAAAGAGGCAAGAGGATCTGTCTGTGAT 360

Qy 361 TGTGGAAGTACCGGAAATTTGTCGACACTGGATATTAGTATTTGCCCGCTCAAGACA 420

Db 361 TGTGGAAGTACCGGAAATTTGTCGACACTGGATATTAGTATTTGCCCGCTCAAGACA 420

Qy 421 TCTATGAAGTTTGTCAAGATGATGATGAGGAAATGAGGAAATGAGGAAATTTCTAC 480

Db 421 TCTATGAAGTTTGTCAAGATGATGATGAGGAAATGAGGAAATGAGGAAATTTCTAC 480

Qy 481 TACATCGTCAGAGAGAGAGACTACAGGATCCCTAACCCACTGACAGGATTCGGGT 540

Db 481 TACATCGTCAGAGAGAGAGACTACAGGATCCCTAACCCACTGACAGGATTCGGGT 540

Qy 541 GGAATGCTAGCCATGCCCAGGATGAAGCTGCGCAACACACTCATCGCTGACTATTTGCC 600

Db 541 GGAATGCTAGCCATGCCCAGGATGAAGCTGCGCAACACACTCATCGCTGACTATTTGCC 600

Qy 601 AAGAGTGGCTTTTCGGGTGTTTCATGCGGTGAATGACCTTGAAGGGAGGACAGTAC 660

Db 601 AAGAGTGGCTTTTCGGGTGTTTCATGCGGTGAATGACCTTGAAGGGAGGACAGTAC 660

Qy 661 ATGTTTCAAGACACACTCCACTGCGAAGCTATAGCAACTGGAATGAGGGGAAACCCAGC 720

Db 661 ATGTTTCAAGACACACTCCACTGCGAAGCTATAGCAACTGGAATGAGGGGAAACCCAGC 720

Qy 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGTCTGGCAGATGAGATGACACA 780

Db 721 GACCCCTATGTCATGAGGACTGTGTGAGATGCTGAGTCTGGCAGATGAGATGACACA 780

Qy 781 GAGTGCCATCTTACCATGTAATTTGCTGTGAGTTCATCAAGAGAAAAAG 831

Db 781 GAGTGCCATCTTACCATGTAATTTGCTGTGAGTTCATCAAGAGAAAAAG 831

RESULT 2

AY409411

LOCUS

DEFINITION Pan troglodytes COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY409411

VERSION AY409411.1

KEYWORDS GI:39765379

SOURCE GSS.

ORGANISM Pan troglodytes (chimpanzee)

REFERENCE

AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Pan.

1 (bases 1 to 834)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE

AUTHORS 2 (bases 1 to 834)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source 1..834

gene

ORIGIN

Query Match 99.0%; Score 823; DB 29; Length 834;

Best Local Similarity 99.4%; Pred. No. 2.2e-216; Indels 0; Gaps 0;

Matches 826; Conservative 0; Mismatches 5;

Qy 1 ATGAATGGCTTTGCAATCCTTCTCGAAGAAACCAATTTATCTCTCTGTTACTATTTCTT 60

Db 1 ATGAATGGCTTTGCAATCCTTCTCGAAGAAACCAATTTATCTCTCTGTTACTATTTCTT 60

Qy 61 TTGCAATTCAGAGTCTGGTCTGGATATGATAGCCCTTACCGCTGAAGTCTGTGCC 120

Db 61 TTGCAATTCAGAGTCTGGTCTGGATATGATAGCCCTTACCGCTGAAGTCTGTGCC 120

Qy 121 ACACACAAATTTTCCAGACCCCAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 180

Db 121 ACACACAAATTTTCCAGACCCCAAGAGAGATGATGTTGAAAAAGAGATCCAGAGAA 180

Qy 181 GAGGAAAGCATGCGAAATGCGACCCATGCGGCGCAAGAGATTAAGAGAACTGGGT 240

Db 181 GAGGAAAGCATGCGAAATGCGACCCATGCGGCGCAAGAGATTAAGAGAACTGGGT 240

Qy 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGGGGTGACAA 300

Db 241 GATATGGAGATCGGGCAATATTTGGCAAGACTGGGCCATTTGGGAAGAGGGGTGACAA 300

Qy 301 GGGGAAAGAGTTTGGTGGAAATGATGAGGAAAGAGGCAAGAGGATCTGTCTGTGAT 360

Db 301 GGGGAAAGAGTTTGGTGGAAATGATGAGGAAAGAGGCAAGAGGATCTGTCTGTGAT 360

Qy 361 TGTGGAAGTACCGGAAATTTGTCGACACTGGATATTAGTATTTGCCCGCTCAAGACA 420

REFERENCE	AUTHORS	TITLE
1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

JOURNAL MEDLINE PUBLISHED 9279253 10349636 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE PUBLISHED 20493374 11042159 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE PUBLISHED 20530913 11078661 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 MEDLINE PUBLISHED 11078661 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE PUBLISHED 11078661 6 (bases 1 to 4591)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Togawa, A., Takanashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
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 QY 187 GAGGCAAGGATGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246
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LOCUS Mus musculus COLEC10 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY409412
VERSION AY409412.1 GI:3976380
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 834)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 834)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 85.9%; Pred. No. 1.6e-166;
Matches 713; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
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ACCESSION BX494095
VERSION BX494095.1 GI:32007261
KEYWORDS EST.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DKFZp779A1511) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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DEFINITION BB612129 RIKEN full-length enriched, 14 days embryo liver Mus
ACCESSION BB612129.1 GI:15394368
VERSION BB612129.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 955)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sugabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
TITLE Yoshihide Hayashizaki
JOURNAL Laboratory for Genome Exploration Research Group, RIKEN Genomic
COMMENT Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/

```

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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K.,
Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTTAAATTAATCCCTCCCTCCCTCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I"
ORIGIN
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Best Local Similarity 81.9%; Pred. No. 1.6e-114;
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DB 69 TTGCAAAATTCAGAGTCTGGGTCTCGATATTGATAGCCGTCTACCGCTGAAGTCTGTGCC 128
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	Matches 438;	Conservative 0;	Mismatches 48;	Indels 0;
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QY	61	TTCGAATTTCAGAGCTTCGGCTTCGGATATTGATACCGCTCTACCGCTGAAGTCGTGGCC	120	
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QY	121	ACACACAAATTTCCACGAGCCCAAGAGAGATGATGTTGAAAAAGGAGATCCACGAGAA	180
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QY	181	GAGGAAAGCATGCGAAAGTGGGAGCGCATGGGGCCGAAAGGAATTAAGGAGAACTCGGT	240
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QY	481	TACATC	486
Db	487	TACATC	492

RESULT 11
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 CF378429
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

CF378429 930 bp mRNA linear EST 27-AUG-2003
 AGNCENT 15349559 NICH D XGC Swb1N Silurana tropicalis cDNA clone
 IMAGE_7005528 5', mRNA sequence.
 CF378429.1 GI:34315873
 EST.
 Silurana tropicalis (western clawed frog)

ORGANISM

Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.

REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

Contact: Daniela S. Gerhard, Ph.D.

JOURNAL

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

COMMENT

Email: cgabbs-remail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM14704 row: j column: 22
High quality sequence stop: 677.

FEATURES

source

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I - oligo(dN) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD XGC Swb1). Library
was constructed by Open Biosystems (Huntsville, AL)."

ORIGIN

Query Match 47.3%; Score 392.8; DB 14; Length 930;
Best Local Similarity 68.7%; Pred. No. 2.6e-97;
Matches 541; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY	44	TCTGTGACTATTCTTTTGGAAATTCAGATCTGGGTCTGGATATTGATAGCGTCTTA	103
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Db	162	CTGTGATACTTGTTCCTCACTCACCAATTCGCGGGACCCAAAGGGATGATGAGA	221
QY	164	AAGGATCAGAGAGAGAGAGATGCGAAGTGGGACGATGGGGCGGAAGAA	223
Db	222	CTGGATACGGGGGTCTTTGGGAAAGCTGGGAAAGATGGAACCCAAAGGGGAGA	281
QY	224	TAAAGGACAACTGGGTGATATGGAGATCGGGGCAATATTGGCAAGACTGGGCC	283
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QY	284	GGAGAGGGTGACAAAGGGGAAAAGTTTCTTGGAAATCTCTGGAGAAAAGGCAAG	343
Db	342	GCAGCAAGGGGATAAGGACATAAAGGCTTCCCGGCTTCCAGGAGGAAAGGAAAT	401
QY	344	CAGGTACTGTCTGTGATCTTGAAGATACCGGAAATTTTGGCAACTGGATATTAGTA	403
Db	402	CAGGCACTTCTGTGATCTTGAAGATACCGGAAATTTTGGCAACTGGATATTAGTA	461
QY	404	TTGCCCGGTCAAGACATCTATGAAGTTTGTCAAGATGTGATACAGGGATTAGGAAA	463
Db	462	TTGCCGACCTAAAGTCTTCTTAAATTTGTAAAAATTTGTAATTTGCCGCAATCAGG	521

QY	464	CTGAGAGAAATTTACTACATCTGTCAGGAGAGAACTACAGGAATCCCTAACCC	523
Db	522	CAGATGAGAGTACTATTATTTGTTGAGAGAGAGCGAACTACAGGATCGCTGACCC	581
QY	524	ACTGAGGATTCGGGGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCA	583
Db	582	AGTGTCCGATAAGAGGGGTACATTTGGCAATGCCCAAGGATCAAGCTACCAATTCCTCA	641
QY	584	TCGCTGACTATTTGCCAAGAGTGGCTCTTTCCGGGTTCATTTGGCGTGAATGACCTTG	643
Db	642	TTGCTGATTCATCTCCAAATGGGGCTTTTCAGATTTATATAGGAATAATGACATTG	701
QY	644	AAAGGGAGGACAGTACATGTTTCAGACACACACTCCCACTGCAGAACTATAGCACTGGA	703
Db	702	AGAAAGAGAGACAGCTTGTGTATGCAGATAACTCCCACTGCAGACTTACAGCAGCTGGA	761
QY	704	ATGAGGGGAGACCCAGGACCCCTATGTCATGAGGACTGTGTGGAGATCTGAGCTCTG	763
Db	762	AAGCCGGAGAACCCCAACGATGGCTCTGGTACGAACTCGGTGGAATGCTCAGCACCG	821
QY	764	GCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAG	823
Db	822	GCCATTGGAACGAGCTGGACTGCACTGTGACCATCTACTTTGTCTGTGAGTTTCTGAAA	881
QY	824	AGAAAAAG 831	
Db	882	AGACAAAG 889	

RESULT 12

LOCUS

DEFINITION

IMAGE:6886251 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Eliot Spindel

cDNA Library Preparation: CLONTECH

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCW3139 row: a column: 02

High quality sequence stop: 526.

FEATURES

source

1. 747

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/clone="IMAGE:6886251"

/tissue_type="Ovary"

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/clone_lib="NICHD Rh Ovl"

/note="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I;

Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.0-4.0 kb. Tissue pooled from

pre-pubertal, post pubertal an menopausal monkeys.

Constructed by Clontech. Note: this is a NICHD Library."

genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0032 row: c column: 3.

FEATURES
source
1. .636
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00321.c.03"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scac)"
/notes="Vector: pT73D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 37.1%; Score 308.4; DB 13; Length 636;
Best Local Similarity 89.0%; Pred. No. 4.9e-74;
Matches 333; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 458 GGGAAACTGAAGAAATTTCTACTACATCGTCAGGAAGAGAACTACAGGGAATCCC 517
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QY 518 TAACCCACTCAGGATTCGGGGTGGAAATGCTAGCCATGCCAAGGATGAAGTCCCAACA 577
Db 61 TGACCCACTCCGGATCCGGGGCGGGATTTAGCCATGCCAAGGACGAAGTCCCAACA 120
QY 578 CACTCATCGTGAATGTTGGCCAGAGTGGTCTTTCCGGTGTTCATTCGGTGTATG 637
Db 121 CGTCTCTCGTGACTAGTCTCCAGAGCGGCTTTTCGAGTGTTCATCGGGGTAAACG 180
QY 638 ACCTTGAAGGGAGGACAGTACATGTTCCACAGACACACTCCACTGCAGAACTATAGCA 697
Db 181 ACCTGGAGAGGGAGGGCCAGTACGTTTCCACAGACACACAGCCACTGCAGAACTACAGCA 240
QY 698 ACTGGAGTGGGGAGACCCAGCCAGCCCTATGGTCATGAGGACTGTGTGAGATGCTGA 757
Db 241 ACTGGCAGGAGGTGAGCCAGCCCTACGGTCAAGGACTGTGTGAAATGCTGA 300
QY 758 GCTCTGCGAGATGGAATGACACAGAGTGGCCATCTTACCATGTACTTTCTGTGAGTTCA 817
Db 301 GCTCGGCGAGATGGAATGACACGGAGTGCCACTGCACATGTACTTTCTGTGAGTTTG 360
QY 818 TCAAGAGAAAG 831
Db 361 TCAAGAGAAAG 374

RESULT 15
BI067078
LOCUS
DEFINITION
pBin.pk010.i8 normalized chicken fat cDNA library Gallus gallus
cDNA clone pBin.pk010.i8 5' similar to gi|5453619 ref|NP_006429.1|
[Homo sapiens] dbj|BA01747.1| (C-type lectin); collectin liver 1
sapiens|G, mRNA sequence.
BI067078
BI067078
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 654)

AUTHORS
TITLE
JOURNAL
COMMENT
Cogburn, L.A., Morgan, R.W. and Burnside, J.
Chicken ESTs from fat
Unpublished (2001)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
1. .654
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
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/clone_lib="normalized chicken fat cDNA library"
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FEATURES
source

ORIGIN

Query Match 36.4%; Score 302.6; DB 12; Length 654;
Best Local Similarity 71.7%; Pred. No. 2e-72;
Matches 386; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
QY 25 CGAAGAAACCAATTTATCTCTGCTGTAATTTCTTTTGAATTCAGAGTCTGGGTCTG 84
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QY 85 GATATTGATAGCCGCTTACCCGCTGAAGTCTGTGCCACACACACAATTTCCACGAGACC 144
Db 175 GATGTTGACATCGACCTTACCAACAGATGTCGTCTGACACACACTATTTTACCTGGACCA 234
QY 145 AAAGAGATGATGTTGAAAGAGAGATCCAGAGAGAGGAGAGATGCGAAGTGGGA 204
Db 235 AAAGGGGATGATGTTGAAAGAGAGATAGAGAGAGTGGGCAACAAAGGAAAGTTGGA 294
QY 205 CGCATGGGGCCGAAAGGAATTAAGGAGAACTGGGTGATATGGGAGATCGGGCAATATT 264
Db 295 CCAAAAGGACCTTAAGGAAACAAAGGAACTGTGGGGATGTCTGGTACCGAGGAATGCTT 354
QY 265 GCACAGACTGGCCCATTTGGGAAGAGGGTGACAAAGGGGAAAAGGTTTGGTTGGATA 324
Db 355 GGGAAAATCGGTCCGATTTGGAGGAAAAGGTGACAAAGGAGCCAAAGGCATATCAGGGGTG 414
QY 325 CCTGAGAGAAAAGGCAAGCAGGTACTGTCTGTGATTGTGGAAGATACCGGAAATTTGTT 384
Db 415 TCTGGAAGAAAAGGAAAGCAGGACAGTCTGTGACTGTGGAGGTACCGCAGAGTTGTT 474
QY 385 GGACAACTGGATATTAGTATTGGCCGGCTCAAGACATCTATGAAAGTTTGTCAAGATGTG 444
Db 475 GGACAACTGAATATCAATGTTGCTCGGCTTAACACATCCATCAAGTTTGTAAAGATGTT 534
QY 445 ATAGCAGGGATTAGGAAACCTGAAGAGAAATTTCTACTATCTATTTCTCAAGAGAGAGAT 504
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QY 505 TACAGGGAAATCCCTAACCCACTGCAGGATTCGGGGTGGAAATGTAGCCATGCCCAAGG 562
Db 595 TACAGAGAAGCCCTGATGATTCATTGCTNNNNNNNNNNNANCACTGGCCCTGCTTAANG 652

Search completed: March 11, 2004, 17:41:14
Job time : 2540 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:11:31 ; Search time 16.6167 Seconds
(without alignments)
584.534 Million cell updates/sec

Title: US-09-600-932-2 COPY 1 46

Perfect score: 228
Sequence: 1 MNGFASLLRRNQFILLVFL.....GLDIDSRPAEVCATHTISP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	228	100.0	277	9	US-09-959-832A-97	Sequence 97, Appl
5	228	100.0	277	10	US-09-978-189-97	Sequence 97, Appl
6	228	100.0	277	10	US-09-978-608A-97	Sequence 97, Appl
7	228	100.0	277	10	US-09-978-585A-97	Sequence 97, Appl
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11	228	100.0	277	10	US-09-999-833A-97	Sequence 97, Appl
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ALIGNMENTS

RESULT 1

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US-09-978-295A-97
/ Sequence 97. Application US/09978295A
/ Patent No. US20020156006A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Flvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Pao, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Scrambled and Trans
/ FILE REFERENCE: P2630P1C1
/ CURRENT APPLICATION NUMBER: US/09/978295A
/ PRIOR FILING DATE: 2001-10-15
/ PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 228; DB 9; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNGFASLLRNQFILLVFLFLLQISGLDIDSRPTAEVCATHHTISP 46
Db      1 MNGFASLLRNQFILLVFLFLLQISGLDIDSRPTAEVCATHHTISP 46

RESULT 2
US-09-978-697-97
; Sequence 97, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 9; Length 277;

Best Local Similarity 100.0%; Pred. No. 6.9e-25; Mismatches 0; Indels 0; Gaps 0;
Matches 46; Conservative 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46

DB 1 MNGFASLLRRNQFILLVFLFIQISGLGIDSRPTAEVCATHHTISP 46

RESULT 3

US-09-978-192A-97

; Sequence 97, Application US/09978192A

; Patent No. US2002017553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

[illegible][illegible]

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Query Match 100.0%; Score 228; DB 9; Length 277;

1 MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISP 46 QV

1 MNGFASLLRRNQFILLVFLFLQIOSLGLDIDSRPTAEVCATHISP 46

RESULT 4

US-09-999-832A-97

Sequence 97, Application US/09999832A
Publication No. US20020192706A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2630P1C63

CURRENT APPLICATION NUMBER: US/09/999,832A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

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PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13

;; PRIOR FILING DATE: 1998-04-22
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Query Match 100.08; Score 228; DB 9; Length 277;
Best Local Similarity 100.08; Pred. No. 6.9e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNGFASLLRRNQFILLVFLVLLQISLGLDIDSRPTAEVCATHTISP 46
DB 1 MNGFASLLRRNQFILLVFLVLLQISLGLDIDSRPTAEVCATHTISP 46

RESULT 5

US-09-978-189-97
; Sequence 97, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084598
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-5-07
PRIOR APPLICATION NUMBER:	60/084627
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PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085339
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PRIOR APPLICATION NUMBER:	60/085323
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085689
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085580
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697
PRIOR FILING DATE:	1998-05-15

Query Match	100.0%;	Score 228;	DB 10;	Length 277;
Best Local Similarity	100.0%;	Pred. No. 6.9e-25;		

1 MNGFASLLRRNQFILLVFLLIQIQLGLDIDSRPTAEVCATHTISP 46
 1 MNGFASLLRRNQFILLVFLLIQIQLGLDIDSRPTAEVCATHTISP 46

RESULT 6

US-09-978-608A-97
; Sequence 97, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm

SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens

US-09-978-608A-97
Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46

RESULT 7

US-09-978-585A-97
; Sequence 97, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm

SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens

US-09-978-585A-97
Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm

SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens

US-09-978-585A-97
Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46

RESULT 8

US-09-978-191A-97
; Sequence 97, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm

SEQ ID NO 97
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens

US-09-978-191A-97
Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46
Db 1 MNGFASLLRRNQFILLVFLFIQISGLGIDISRPTAEVCATHHTISP 46

PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
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PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
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PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13

;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;

Best Local Similarity 100.0%; Pred. No. 6.9e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLLIQSLGLDIDSRPTAEVCATHHTISP 46

Db 1 MNGFASLLRRNQFILLVFLLIQSLGLDIDSRPTAEVCATHHTISP 46

RESULT 9

US-09-978-403A-97

; Sequence 97, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR APPLICATION NUMBER: 60/085689
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25; Indels 0; Caps 0;
Matches 46; Conservative 0; Mismatches 0;

QY 1 MNGFASLIRRNQFILLVFLIIQSLGLDIDSRPTAEVCATHTISP 46
DB 1 MNGFASLIRRNQFILLVFLIIQSLGLDIDSRPTAEVCATHTISP 46

RESULT 10

US-09-978-564A-97
; Sequence 97, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/077641

PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
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PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.08; Score 228; DB 10; Length 277;
Best Local Similarity 100.08; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFIQISLGLDIDSRPTAEVCATHITSP 46
DB 1 MNGFASLLRRNQFILLVFLFIQISLGLDIDSRPTAEVCATHITSP 46

RESULT 11
US-09-999-833A-97
; Sequence 97, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hylan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
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; PRIOR FILING DATE: 1998-03-13

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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 228; DB 10; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.9e-25;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNGFASLIRRNQFILLVFLIIQSLGLDIDSRPTAEVCATHTISP 46
 Db 1 MNGFASLIRRNQFILLVFLIIQSLGLDIDSRPTAEVCATHTISP 46
 RESULT 12
 US-09-981-915A-97
 ; Sequence 97, Application US/09981915A
 ; Publication No. US20030054986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C12
 ; CURRENT APPLICATION NUMBER: US/09/981,915A
 ; CURRENT FILING DATE: 2001-10-16
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 228; DB 10; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.9e-25;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MNGFASLRNRQFILLVLFIQIQLGIDISRPTEVCATHTISP 46
 DB 1 MNGFASLRNRQFILLVLFIQIQLGIDISRPTEVCATHTISP 46

RESULT 13

US-09-978-824-97

; Sequence 97, Application US/09978824

; Publication No. US20030055216A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P/C14

; CURRENT APPLICATION NUMBER: US/09/978,824

; CURRENT FILING DATE: 2001-10-17

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
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; PRIOR FILING DATE: 1998-04-21
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; PRIOR FILING DATE: 1998-04-29
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;; PRIOR FILING DATE: 1998-04-29
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Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6,9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MNGPASHLRNQIFLLVFLFQIQSLGLDIDSRPTAEVCATHTTSP 46
Db 1 MNGPASHLRNQIFLLVFLFQIQSLGLDIDSRPTAEVCATHTTSP 46

RESULT 14

US-09-918-585A-97
; Sequence 97, Application US/09918585A
; Publication No. US2003060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C1
;; CURRENT APPLICATION NUMBER: US/09/918,585A
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. NO. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNGFASLLRRNQFILLVLFLQIQSLGLDIDSDRPTAEVCATHTISP 46

RESULT 15
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; Sequence 97, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978,423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 228; DB 10; Length 277;
Best Local Similarity 100.0%; Pred. No. 6.9e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNGFASLRRNQFILLVFLFIQSLGLDIDSRPTAEVCATHTISP 46
Dd 1 MNGFASLRRNQFILLVFLFIQSLGLDIDSRPTAEVCATHTISP 46

Search completed: March 8, 2004, 12:18:56
Job time : 17.6167 secs

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: March 8, 2004, 11:56:05 ; Search time 7.29515 Seconds
(without alignments)

328.331 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46

Perfect score: 228

Sequence: 1 MNGFASLLRNQFILLVFL.....GLDIDSPRTAEVCATHHTISP 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	DB ID	Description
1	55	24.1	313	1	OAK1_HUMAN	Q8NGX5 homo sapien
2	52	22.8	130	1	OREX_MOUSE	O55241 mus musculus
3	52	22.8	130	1	OREX_RAT	O55232 rattus norv
4	51	22.4	77	1	SECQ_MYCGE	P58061 mycoplasma
5	51	22.4	1077	1	B2K3_CABEL	Q19192 caenorhabdi
6	50.5	22.1	331	1	RESR_HAEIN	P44329 haemophilus
7	50.5	22.1	372	1	S17B_HUMAN	O94768 homo sapien
8	50	21.9	168	1	X027_RAT	P75084 mycoplasma
9	50	21.9	281	1	CD37_RAT	P31053 rattus norv
10	50	21.9	817	1	FTSK_BRUME	O8YJb8 bruceella me
11	50	21.9	854	1	FTSK_BRUSU	O8FY10 bruceella su
12	49.5	21.7	182	1	YLH9_CABEL	P34363 caenorhabdi
13	49	21.5	105	1	P679_TREPA	O83685 treponema p
14	49	21.5	484	1	PER2_VOLCA	P81132 volvox cart
15	48.5	21.3	228	1	COX2_AEDAE	P50892 aedes aegypt
16	48.5	21.3	228	1	COX2_CULQU	P50893 culicx quinq
17	48.5	21.3	747	1	Y030_UREPA	O9PRB5 ureaplasma
18	48	21.1	259	1	UPKB_MUSVI	P30413 mustela vis
19	48	21.1	1118	1	PHY_ADICA	P42496 adiantum ca
20	47.5	20.8	134	1	ATPE_CHLVU	P32979 chlorella v
21	47.5	20.8	318	1	BST1_HUMAN	Q10588 homo sapien
22	47.5	20.8	349	1	OPSG_CARAU	P32311 caecilius a
23	47.5	20.8	360	1	NSR2_CABEL	P34889 caenorhabdi
24	47.5	20.8	715	1	NSR1_PSEAE	O9HY13 pseudomonas
25	47.5	20.8	807	1	YB9T_YEAST	P38148 saccharomyc
26	47.5	20.8	2703	1	NOTC_DROME	P07207 drosophila
27	47	20.6	76	1	SECQ_MYCPN	O9EXD0 mycoplasma
28	47	20.6	166	1	YA43_HAEIN	P44101 haemophilus
29	47	20.6	214	1	VENI_YEREN	P52388 yersinia en
30	47	20.6	282	1	AURC_MOUSE	O88445 mus musculus
31	47	20.6	309	1	AURC_HUMAN	O9UQb9 homo sapien
32	47	20.6	319	1	BST1_RAT	O63072 rattus norv
33	47	20.6	376	1	CPR2_ARATH	Q91XW3 arabidopsis

RESULT 1

ID	OAK1_HUMAN	STANDARD;	PRT;	313 AA.
AC	Q8NGX5;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DB	Olfactory receptor 10K1.			
GN	OR10K1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Putative odorant receptor.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
CC	-!- DATABASE: NAME=Human Olfactory Receptor Data Explorer (HORDE);			
CC	MW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbols			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AB065641; BAC05867.1; --			
DR	Genew; HGNC:14693; OR10K1.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOPOPSN.			
DR	PROSITE; PS00237; G-PROTEIN RECP F1.1; FALSE_NEG.			
DR	PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN 1 25			
FT	TRANSMEM 26 46			
FT	DOMAIN 47 54			
FT	TRANSMEM 55 75			
FT	DOMAIN 76 99			
FT	TRANSMEM 100 120			
FT	DOMAIN 121 139			
FT	TRANSMEM 140 160			
FT	DOMAIN 161 197			
FT	TRANSMEM 198 217			
FT	DOMAIN 218 237			
FT	TRANSMEM 238 258			
FT	DOMAIN 259 271			
FT	EXTRACELLULAR (POTENTIAL).			
FT	1 (POTENTIAL).			
FT	2 (POTENTIAL).			
FT	3 (POTENTIAL).			
FT	4 (POTENTIAL).			
FT	5 (POTENTIAL).			
FT	6 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.P., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=98081872; PubMed=9419374;
RX de Lecea L., Kilduff T.S., Peyron C., Gao X.-B., Foye P.E.,
RX Danielson P.E., Fukuhara C., Battenberg E.L.F., Gautvik V.T.,
RX Bartlett F.S. II, Frankel W.N., van den Pol A.N., Bloom F.E.,
RX Gautvik K.M., Sutcliffe J.G.;
RT "The hypocretins: hypothalamus-specific peptides with neuroexcitatory
RT activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:322-327(1998).
RN [3]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621;
RX Hungs M., Mignot E.;
RX "Hypocretin/orexin, sleep and narcolepsy.";
RT Biossays 23:397-406(2001).
RN [4]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RX Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RX "To eat or to sleep? Orexin in the regulation of feeding and
RX wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
RN [5]
RP -|- FUNCTION: Neuropeptides that play a significant role in the
RP regulation of food intake and sleep-wakefulness, possibly by
RP coordinating the complex behavioral and physiologic responses of
RP these complementary homeostatic functions. A broader role in the
RP homeostatic regulation of energy metabolism, autonomic function,
RP hormonal balance and the regulation of body fluids, is also
RP suggested. A modulation effect on luteinizing hormone-releasing
RP hormone (LHRH) secretion also suggests a more minor contribution
RP to the regulation of reproductive function. Orexin-A binds to both
RP OX1R and OX2R with a high affinity, whereas orexin-B binds only to
RP OX2R with a similar high affinity.
RP -|- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
RP RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
RP SYNAPSES.
RP -|- TISSUE SPECIFICITY: Produced by a small group of neurons
RP restricted to the lateral and posterior hypothalamus and
RP perifornical areas. Positive neurons project widely throughout the
RP entire neuroaxis. Particularly abundant projections in the
RP cerebral cortex, olfactory bulb, hippocampus, amygdala, septum,
RP diagonal band of Broca, bed nucleus of the stria terminalis,
RP thalamus, anterior and posterior hypothalamus, midbrain,
RP brainstem, and spinal cord. Immunoreactivity reported in the
RP enteric nervous system and pancreas. In small amount, also
RP detected in the testis.
RP -|- DEVELOPMENTAL STAGE: DETECTED AS EARLY AS EMBRYONIC DAY 18, BUT
RP EXPRESSION INCREASED DRAMATICALLY AFTER THE THIRD POSTNATAL WEEK.
RP -|- INDUCTION: By nutritional state, up-regulated by fasting, fluid
RP deprivation and insulin-induced hypoglycemia. Orexin-A
RP immunoreactivity varies diurnally and peaks during the dark
RP phase, in the pons and the location of locus coeruleus.
RP -|- PTM: Specific enzymatic cleavages at paired basic residues yield
RP the different active peptides.
RP -|- MASS SPECTROMETRY: MW=3558.7; MW_ERR=0.1; METHOD=MALDI;
RP RANGES=33-65.
RP -|- SIMILARITY: Belongs to the orexin family.
RP -|- DATABASE: NAME-Protein Spotlight;
RP NOTE=Issue 15 of October 2001;
RP WWW="http://www.expasy.org/spotlight/articles/sptl015.html".
RN [6]
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CC -----
CC EMBL: AF041241; AAC40039.1; -;
CC EMBL: AF019565; AAC02933.1; -;
CC InterPro: IPR001704; Orexin.
CC Pfam: PF02072; Orexin; 1.
CC PRINTS: PR01091; OREXINPP.
CC KW Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation;
CC PYRROLIDONE CARBOXYLIC ACID.
CC FT SIGNAL 1 32
CC FT PEPTIDE 33 65 OREXIN-A.
CC FT PEPTIDE 69 96 OREXIN-B.
CC FT PROPEP 97 130
CC FT MOD RES 33 33 PYRROLIDONE CARBOXYLIC ACID.
CC FT MOD RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).
CC FT MOD RES 96 96 AMIDATION (G-97 PROVIDE AMIDE GROUP).
CC FT DISULFID 38 44
CC FT DISULFID 39 46
CC SQ SEQUENCE 130 AA; 13645 MW; 00CAB259EDF2A404 CRC64;
CC
CC Query Match 22.8%; Score 52; DB 1; Length 130;
CC Best Local Similarity 38.7%; Pred. No. 3.8;
CC Matches 12; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
CC
CC QY 15 LVLVFLQLQISGLDIDSRPTAEVCATHIS 45
CC DB 15 LLLLLLPPALLSLGVDAQPLDCCRQKTC 45
CC
CC RESULT 4
CC SECG MYCGE STANDARD; PRT; 77 AA.
CC ID SECG MYCGE STANDARD; PRT; 77 AA.
CC AC PS8061; 2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Probable protein-export membrane protein secg.
CC GN SECG OR MG103.1.
CC OS Mycoplasma genitalium.
CC OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CC CX NCBI_TaxID=2097;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX STRAIN=ATCC 33530 / G-37;
CC RX MEDLINE=96026346; PubMed=7569993;
CC RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
CC RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
CC RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.D.,
CC RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
CC RA Tomb J.-F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
CC RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
CC RT "The minimal gene complement of Mycoplasma genitalium.";
CC RL Science 270:397-403(1995).
CC RN [2]
CC RP IDENTIFICATION.
CC RP Medigue C., Bocs S.;
CC RL Unpublished observations (MAY-2001).
CC CC -|- FUNCTION: Involved in protein export. Participates in an early
CC event of protein translocation (By similarity).
CC CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC CC -|- SIMILARITY: Belongs to the secg family.
CC -----
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CC -----

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodok A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.,
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.",
RL Science 269:496-512(1995).
CC -!- FUNCTION: Transcriptional repressor for the ribose rbsDACBK operon
CC (By similarity).
CC -!- SIMILARITY: Contains 1 HTH lacI-type DNA-binding domain.
CC
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CC
CC EMBL: U32732; AAC22164.1; -
CC F01R; C64073; C64073.
CC HSSP: P15039; IPRU.
CC TIGR: H10506; -
CC InterPro: IPR000843; HTH LacI.
CC InterPro: IPR001761; PeriplaBP/LacI.
CC Pfam: PF00356; lacI, 1.1.1.1.
CC Pfam: PF00352; PeriplaBP-like, 1.
CC PRINTS: PR00036; HTHLACI.
CC SMART: SM00354; HTH LACI, 1.
CC PROSITE: PS00356; HTH LACI, 1.
CC PROSITE: PS00352; HTH LACI, 1.
CC PROSITE: PS00354; HTH LACI, 1.
CC Transcription regulation; Repressor; DNA-binding; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 55 HTH LACI-TYPE.
FT DOMAIN 3 22 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 331 AA; 36594 MW; 4034AD4A53ED1E5 CRC64;
Query Match 22.1%; Score 50.5; DB 1; Length 331;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 8; Indels 1; Gaps 1;
QY 20 LLIQISGLDIDSRPTAVFCGTHHIS 45
Db 223 VLGIQSL-LTQSRPTAVFCGTHHIS 247
RESULT 7
S17B_HUMAN STANDARD; PRT; 372 AA.
AC O94768;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Serine/threonine protein kinase 17B (EC 2.7.1.37) (DAP kinase-related
DE apoptosis-inducing protein kinase 2).
GN SKI17B OR DRAK2.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND MUTAGENESIS OF LYS-62.
RC TISSUE=Liver, and Placenta;
RX MEDLINE=99003259; PubMed=9786912;
RA Sanjo H., Kawai T., Akira S.,
RT "DRAKs, novel serine/threonine kinases related to death-associated
RT protein kinase that trigger apoptosis.",
RL J. Biol. Chem. 273:29062-29071(1998).
RN [2]

RP SEQUENCE FROM N.A.
RX TISSUE=B-Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Klausner R.D., Fellers K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Acts as a positive regulator of apoptosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with CHP causing CHP to translocate from the
CC Golgi to the nucleus (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, lung, pancreas.
CC -!- Lower levels in heart, brain, liver, skeletal muscle and kidney.
CC -!- PTM: Autophosphorylation.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. DAP
CC kinase subfamily.
CC
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CC
CC EMBL: AB011421; BAA34127.1; -
CC EMBL: BC016040; AAH16040.1; -
CC HSSP: Q63450; IAO6.
CC GeneW: HGNC:11396; STK17B.
CC MIN: 604727; -
CC GO: GO:0005634; C:nucleus; TAS.
CC GO: GO:0004674; F:protein serine/threonine kinase activity; TAS.
CC GO: GO:0006917; P:induction of apoptosis; TAS.
CC GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR008271; Ser_thr_pkin_AS.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD00001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation; Nuclear protein; Apoptosis.
CC DOMAIN 33 293 PROTEIN_KINASE.
CC DOMAIN 308 311 POLY-SER.
CC NP_BIND 39 47 ATP (BY SIMILARITY).
CC BINDING 62 62 ATP.
CC ACT_SITE 158 158 BY SIMILARITY.
CC MUTAGEN 62 62 K->A: LOSS OF ACTIVITY AND OF
CC APOPTOTIC FUNCTION.
SQ SEQUENCE 372 AA; 42344 MW; 7E69FFAED6D1FF3 CRC64;
Query Match 22.1%; Score 50.5; DB 1; Length 372;
Best Local Similarity 50.0%; Pred. No. 18;

Matches 11; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 23 IQSLGL-DIDGRPAEVCATHT 43
||| : : : ||| : : :
Db 270 IQSLLVKPKPEKPAEICLSHS 291
||| : : : ||| : : :
RESULT 8
Y027 MYCPN
ID Y027 MYCPN STANDARD; PRT; 168 AA.
AC P75084;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG027 homolog (B01_orf168).
GN MN030 OR MP124.
OS Mycoplasma pneumoniae.
CX Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Piagens H., Pirkl E., Li B.-C.,
RA Herkmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
CC EMBL; AB000015; AAB95772.1; -.
DR PIR; S73450; S73450.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 168 AA; 19214 MW; C37192BBA3A82D4B CRC64;

Query Match 21.9%; Score 50; DB 1; Length 168;
Best Local Similarity 39.6%; Pred. No. 9.5;
Matches 19; Conservative 2; Mismatches 13; Indels 14; Gaps 3;

QY 1 MNGFASLLRNQ-----FILLVFL--QISGLDID--SRP 34
||| : : : ||| : : :
Db 22 VNGTTSKLTQRTQRTAIVEIFATLFLPKTADQIQAFLLDYDVP 69
||| : : : ||| : : :
RESULT 9
CD37 RAT
ID CD37 RAT STANDARD; PRT; 281 AA.
AC P31053;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukocyte antigen CD37.
GN CD37.
OS Rattus norvegicus (Rat).
CX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EVG X DA;
RX MEDLINE=90354767; PubMed=2388030;
RA Classon B.J., Williams A.F., Willis A.C., Seed B., Stamenkovic I.;
RT "The primary structure of the human leukocyte antigen CD37, a species
RT homologue of the rat MRC OX-44 antigen."
RL J. Exp. Med. 172:1007-1007(1990).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: B lymphocytes.
CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
CC -----
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CC -----
CC EMBL; X53517; CAA37596.1; -.
DR PIR; B47629; B47629.
DR InterPro; IPR00301; Transmem 4.
DR Pfam; PF00335; Transmembrane; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Glycoprotein; Antigen; Transmembrane.
NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonowski L., Larsen N., D'Souza M., Bernal A., Marz M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: DNA motor protein, which is both required to move DNA
CC out of the region of the septum during cell division and for the
CC septum formation. Tracks DNA in an ATP-dependent manner by
CC generating positive supercoils in front of it and negative
CC supercoils behind it (By similarity).
CC -!- SUBUNIT: Homodimer. This suggests the formation of a ring
CC between the two cells at the septum that surrounds DNA (By

Query Match 21.9%; Score 50; DB 1; Length 281;
Best Local Similarity 47.8%; Pred. No. 16;
Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 18 LFLQISGLDIDSRPAEVC 40
||| : : : ||| : : :
Db 196 LFLQSLRLGFRALRQTADICA 218
||| : : : ||| : : :
RESULT 10
FTSK BRUME
ID FTSK BRUME STANDARD; PRT; 817 AA.
AC Q8XJB8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA translocase ftsK.
GN FTSK OR BME10168.
OS Brucella melitensis.
CX Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonowski L., Larsen N., D'Souza M., Bernal A., Marz M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: DNA motor protein, which is both required to move DNA
CC out of the region of the septum during cell division and for the
CC septum formation. Tracks DNA in an ATP-dependent manner by
CC generating positive supercoils in front of it and negative
CC supercoils behind it (By similarity).
CC -!- SUBUNIT: Homodimer. This suggests the formation of a ring
CC between the two cells at the septum that surrounds DNA (By

RT elegans. ";

RL Nature 368:32-38(1994).

CC -----

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CC -----

CC EMBL; Z29117; CAA82381.1; -.

DR PIR; S40729; S40729.

DR WormPep; C48B4.9; CRO0485.

KW Hypothetical protein.

SQ SEQUENCE 182 AA; 20971 MW; 398111F21FEBDA42 CRC64;

Query Match 21.7%; Score 49.5; DB 1; Length 182;

Best Local Similarity 27.7%; Pred. No. 12; Indels 13; Gaps 2;

Matches 13; Conservative 9; Mismatches 12; Indels 13; Gaps 2;

QY 13 FILVLFLQLQSL-----GLDIDS-----RPTAEVCATHITSP 46

Db 126 FILVILLAVAGSYTWLCHLLIEGLDENAPKRSPOCKICSNHYVP 172

RESULT 13

Y679 TREPA STANDARD; PRT; 105 AA.

AC O83685;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein TP0679.

GN TP0679.

OS Treponema pallidum.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=160;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Nichols;

RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,

RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,

RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,

RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,

RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,

RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis

RT spirochete."

RL Science 281:375-388(1998).

CC -----

CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -----

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CC -----

CC EMBL; AE001242; AAC6555.1; -.

DR PIR; G71294; G71294.

DR TIGR; TP0679; -.

KW Hypothetical protein; Transmembrane; Complete proteome.

FT TRANSMEM 14 34 POTENTIAL.

FT TRANSMEM 41 61 POTENTIAL.

FT TRANSMEM 80 100 POTENTIAL.

SQ SEQUENCE 105 AA; 11586 MW; 068BADC2502523C CRC64;

Query Match 21.5%; Score 49; DB 1; Length 105;

Best Local Similarity 65.0%; Pred. No. 8.1;

Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MNGFASLLRNQFILLVFL 20

Db 1 MNEFLSLLSRAQTILLMLRL 20

RESULT 14

PER2 VOLCA STANDARD; PRT; 484 AA.

AC P81132;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Perphorin II (Fragment).

OS Volvox carteri.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OX Volvocaceae; Volvox.

OX NCBI_TaxID=3067;

RN (1)

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13; 182-215 AND 413-441.

RX MEDLINE=93209229; PubMed=8458341;

RA Sumper M., Berg E., Wenzl S., Godl K.;

RT "How a sex pheromone might act at a concentration below 10(-16) M.";

RL EMO J. 12:831-836(1993).

CC -|- FUNCTION: May be involved in conversion of asexual males and

CC females to the sexual pathway.

CC -|- SUBCELLULAR LOCATION: Extracellular matrix.

CC -|- INDUCTION: By sexual inducer glycoprotein.

CC -----

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CC -----

CC EMBL; X69802; CAB56809.1; -.

DR PIR; S36339; S36339.

KW Extracellular matrix; Glycoprotein; Multigene family.

FT NONTER 1

FT DOMAIN 173 177 POLY-PRO.

FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 484 AA; 50960 MW; 0733618764BB2345 CRC64;

Query Match 21.5%; Score 49; DB 1; Length 484;

Best Local Similarity 45.5%; Pred. No. 39;

Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 20 LQIQSLGLDIDSRPTAEVCAT 41

Db 103 VLRLTQLGLDTTAAQDAEVLCT 124

RESULT 15

COX2_AEDAE STANDARD; PRT; 228 AA.

AC P50692;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).

GN COII.

OS Aedes aegypti (Yellowfever mosquito).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Koashiung;
RX MEDLINE=95333127; PubMed=7608924;
RA Ho C.M., Liu Y.M., Wei Y.H., Hu S.T.;
RT "Gene for cytochrome c oxidase subunit II in the mitochondrial DNA of
RL Culex quinquefasciatus and Aedes aegypti (Diptera: Culicidae).";
CC J. Med. Entomol. 32:174-180(1995).
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the bimetallic center of the catalytic subunit 1.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- COFACTOR: Copper A.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC -----
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CC -----
DR EMBL; L34412; AAA9168.1; -.
DR HSP; P18400; ICYX.
DR InterPro; IPR001505; Copper_CuA.
DR InterPro; IPR008972; CupredOxin.
DR InterPro; IPR002429; Cyt_c_ox_2.
DR Pfam; PF00116; COX2; 1.
DR Pfam; PF02790; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASEII.
DR ProDom; PD000131; Copper_CuA; 1.
DR PROSITE; PS00078; COX2; 1.
KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
KW Electron transport; Respiratory chain.
FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT TRANSMEM 27 48 POTENTIAL.
FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).
FT TRANSMEM 63 82 POTENTIAL.
FT DOMAIN 83 228 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT METAL 161 161 COPPER A (PROBABLE).
FT METAL 196 196 COPPER A (PROBABLE).
FT METAL 200 200 COPPER A (PROBABLE).
FT METAL 204 204 COPPER A (PROBABLE).
SQ SEQUENCE 228 AA; 26481 MW; 0D69A2DCAA788789 CRC64;
Query Match 21.3%; Score 48.5; DB 1; Length 228;
Best Local Similarity 25.3%; Pred. No. 21;
Matches 20; Conservative 8; Mismatches 18; Indels 33; Gaps 3;
QY 1 MNGFASLLRRNQFILL-----VLELLQIQSLGIDIDSRP----- 34
Db 130 LMGFRLLVDVNRILPMNNQIRILVTATDVLSHTVPSLGKVIDATPGRLNQTNFLINQP 189
QY 35 -----TAEYC-ATHTISP 46
Db 190 GLFFGQCSEICGNHSP 208

Search completed: March 8, 2004, 12:12:06
Job time : 8.29515 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2004, 12:02:31 ; Search time 35.2599 Seconds
(without alignments)
411.624 Million cell updates/sec

Title: US-09-600-932-2_COPY_1_46

Perfect score: 228
Sequence: 1 MNGFASILRRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	100.0	277	4	Q9V627
2	162	71.1	277	11	Q8C1C5
3	159	65.7	277	11	Q8C1C5
4	59	25.9	320	16	Q7V514
5	57	25.0	534	16	Q8E272
6	56.5	24.8	460	16	Q8F9X2
7	55.5	24.3	272	16	Q8DVK0
8	55	24.1	159	5	Q8I189
9	55	24.1	362	16	Q98218
10	54.5	23.9	228	8	Q98813
11	54	23.7	261	4	Q8NGX4
12	54	23.7	473	5	Q86JY9
13	54	23.7	1419	5	Q8IAX3
14	53.5	23.5	483	4	Q9V6V7
15	53.5	23.5	504	16	Q92KV3
16	53	23.2	268	4	Q9H670

17	53	23.2	304	4	Q9H079
18	53	23.2	339	5	Q8SW71
19	53	23.2	386	16	Q8YWS7
20	53	23.2	788	16	Q882Q7
21	52.5	23.0	173	2	O51892
22	52.5	23.0	228	8	O48399
23	52.5	23.0	228	8	O48312
24	52.5	23.0	228	8	O47820
25	52.5	23.0	228	8	O47822
26	52.5	23.0	228	8	O47818
27	52.5	23.0	228	8	O47821
28	52.5	23.0	228	8	O47819
29	52.5	23.0	228	8	O48360
30	52.5	23.0	228	8	O48323
31	52.5	23.0	228	8	O47823
32	52.5	23.0	228	8	O48283
33	52.5	23.0	597	16	O51037
34	52	22.8	137	2	O68055
35	52	22.8	162	4	O9NFI0
36	52	22.8	221	16	Q892S4
37	52	22.8	258	11	Q8BXS3
38	52	22.8	433	16	Q9PE45
39	52	22.8	433	16	Q87E54
40	52	22.8	435	5	Q9Y016
41	52	22.8	477	5	Q22532
42	52	22.8	562	11	Q8BXL9
43	52	22.8	794	5	Q9V4X7
44	52	22.8	794	5	O96648
45	52	22.8	820	5	Q9V4X6

ALIGNMENTS

RESULT 1

Q9V627 PRELIMINARY; PRT; 277 AA.
AC Q9V627;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Collectin 34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9240768; PubMed=10224141;
RA Ohtani K., Suzuki Y., Eda S., Kawai T., Kase T., Yamazaki H.,
RA Kashi H., Sakai Y., Fukuchi A., Sakamoto T., Wakamiya N.;
RT "Molecular cloning of a novel collectin from liver (CL-L1).";
RL J. Biol. Chem. 274:13681-13689(1999).
DR EMBL; AB002631; BAA81747.1; -;
DR HSSP; P19999; 2MSB.
DR Genew; HGNC:2220; COLEC10.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005530; F:lectin; TAS.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; Lactin; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
SQ SEQUENCE 277 AA; 30733 MW; 9736861CEBDC5C25 CRC64;

Query Match 100.0%; Score 228; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFASILRRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46
|||||

```
Db 1 MNGFASLLRRNQFILLVFLFLLQISLGLDIDSRPTAEVCATHHTISP 46
RESULT 2
Q8CFC5 PRELIMINARY; PRT; 277 AA.
ID Q8CFC5
AC Q8CFC5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin 34 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RC MEDLINE=22354583; PubMed=12466851;
RA THE FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK028423; BAC25941.1; -
DR GO; GO:0005523; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR SEQUENCE 277 AA; 30510 MW; 945F23A2E5404872 CRC64;

Query Match 71.1%; Score 162; DB 11; Length 277;
Best Local Similarity 73.9%; Pred. No. 9.1e-15;
Matches 34; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFLLQISLGLDIDSRPTAEVCATHHTISP 46
Db 1 MNGFVLLRSNLSMLVLLALLHFSQSLGLDVSRAAEVCATHHTISP 46

RESULT 3
Q8CF98 PRELIMINARY; PRT; 277 AA.
ID Q8CF98
AC Q8CF98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Collectin-L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL 6J; TISSUE=Liver;
RC MEDLINE=22333927; PubMed=12450124;
RA Kawai T., Suzuki Y., Eda S., Kase T., Ohtani K., Sakai Y., Keeshi H.,
RA Fukuchi A., Sakamoto T., Nozaki M., Copeland N.G., Jenkins N.A.,
RA Wakamiya N.;
RT "Molecular Cloning of Mouse Collectin Liver 1.";
RL Biosci. Biotechnol. Biochem. 66:2134-2145 (2002).
DR EMBL; AB016429; BAC53954.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR001304; Lectin.C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00059; lectin.c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
```

```
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 277 AA; 30524 MW; 98C743A2E07A2872 CRC64;

Query Match 69.7%; Score 159; DB 11; Length 277;
Best Local Similarity 71.7%; Pred. No. 2.4e-14;
Matches 33; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLFLLQISLGLDIDSRPTAEVCATHHTISP 46
Db 1 MNGFVLLRSNLSMLVLLALLHFSQSLGLDVSRAAEVCATHHTISP 46

RESULT 4
QV7514 PRELIMINARY; PRT; 320 AA.
ID QV7514
AC QV7514;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycosyl transferase, family 2.
GN Pfl1766.
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
OC Prochlorococcus.
CX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047 (2003).
DR EMBL; BX572100; CAZ21941.1; -
RW Transferase; Complete proteome.
SQ SEQUENCE 320 AA; 35561 MW; 0009549536C93698 CRC64;

Query Match 25.9%; Score 59; DB 16; Length 320;
Best Local Similarity 40.6%; Pred. No. 5.3;
Matches 13; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 3 GFASLLRRNQFILLVFLFLLQISLGLDIDSRP 34
Db 239 GFGLLAWGGSLTSTIYLLAIAKLMGEDIGNRP 270

RESULT 5
Q8EZ72 PRELIMINARY; PRT; 534 AA.
ID Q8EZ72
AC Q8EZ72;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transcriptional regulator, Arac family.
GN LA3986.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
CX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011553; AAN51184.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH Arac; 1.
DR PRINTS; PR00032; HTHARAC.
```

[illegible]


```
RESULT 12
Q86JY9 Q86JY9 PRELIMINARY; PRT; 473 AA.
AC Q86JY9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Dictyostelium discoideum (Slime mold). Ras-related protein
DE RabA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RT Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; AAO51356.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003928; F:RAS small monomeric GTPase activity; IEA.
DR GO; GO:0003930; F:RAS small monomeric GTPase activity; IEA.
DR GO; GO:0003931; F:Rho small monomeric GTPase activity; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR003577; GTPase_Ras.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR01806; Ras trnsfrmg.
DR InterPro; IPR02078; Sig54 interact.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTNSFRMG.
DR SMART; SM00175; RAB; 1.
DR SMART; SM00173; RAS; 1.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
DR PROSITE; PS00675; SIGMA54 INTERACT 1; 1.
SQ SEQUENCE 473 AA; 54662 MW; 6456F43077B5573E CRC64;

Query Match 23.7%; Score 54; DB 5; Length 473;
Best Local Similarity 32.4%; Pred. No. 41;
Matches 11; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 11 NQFLLVFLQIQSLGIDSRPTAEVCATHI 44
DB 5 NLFILICFYINYSIGADRNFFINEILAKSI 38

RESULT 13
Q81AX3 Q81AX3 PRELIMINARY; PRT; 1419 AA.
AC Q81AX3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN PF08_0078.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 23.5%; Score 53.5; DB 4; Length 483;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51237.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA ATPase.
DR Pfam; PF00005; ABC tran; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 1419 AA; 170107 MW; 7E481EDA8E3A0A8 CRC64;

Query Match 23.7%; Score 54; DB 5; Length 1419;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNGFASLLRRNQFILLVFLQIQSLGIDSRPT 35
DB 343 LNTLSSSVKNDFTLLYKILSYMKNGIELSLNPT 377

RESULT 14
Q9Y6V7 Q9Y6V7 PRELIMINARY; PRT; 483 AA.
ID Q9Y6V7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR R27090.2 (Hypothetical protein).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RT "Sequence analysis of an ~1 Mb region containing the MEF2B gene in
RT 19p13.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
DR EMBL; AC002985; AAB81544.1; -
DR EMBL; BC002674; AAH02674.1; -
DR HSP; Q58083; 1HV8.
DR Genew; HGNC:18684; DDX49.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR000629; DEAD_box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW Hypothetical protein; ATP-binding; Helicase; Hydrolase.
OX NCBI_TaxID=9606;
SQ SEQUENCE 483 AA; 54226 MW; 2B46DD6A992B532 CRC64;

Query Match 23.5%; Score 53.5; DB 4; Length 483;
```

Best Local Similarity 35.9%; Pred. No. 49;
Matches 14; Conservative 5; Mismatches 17; Indels 3; Gaps 1;

QY 4 FASLLRNQFILLVFLQLQISLGIDSDSPRTAEVCATH 42
Db 288 FAALAKFKSSIVRIIATDVASRGLDI---PTVQVINH 323

RESULT 15

Q92KV3 PRELIMINARY; PRT; 504 AA.
AC Q92KV3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein R00037.
GN R00037 OR SMC02757.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Furnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591782; CAC41424.1; -.
DR InterPro; IPR003442; UPF0079.
DR Pfam; PF02367; UPF0079; 1.
DR TIGRFAMs; TIGR00150; TIGR00150; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 504 AA; 56713 MW; 255569A6CDADCDOE CRC64;

Query Match 23.5%; Score 53.5; DB 16; Length 504;
Best Local Similarity 36.4%; Pred. No. 52;
Matches 16; Conservative 6; Mismatches 11; Indels 11; Gaps 2;

QY 5 ASILLRNQFILLVLF-----LLOIQSLG-----LDIDSRTAE 37
Db 228 SQLRKRGFAPAIYARDLDQGLLIENLSEGLDIDGRPAE 271

Search completed: March 8, 2004, 12:15:10
Job time : 37.2599 secs

Use for Registration

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: March 8, 2004, 12:03:01 ; Search time 12.1586 Seconds
(without alignments)
363.925 Million cell updates/sec

title: US-09-600-932-2_COPY_1_46
effect score: 228
sequence: 1 MNGFASLLRRNQFILLVFL.....GLDIDSRPTAEVCATHITSP 46

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters: 283366

inimum DB seq length: 0
aximum DB seq length: 2000000000
ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR_78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	ID	Description
1	159	69.7	277	JC7903	collectin liver 1
2	53	23.2	386	AE1996	hypothetical prote
3	52.5	23.0	597	D70100	phosphoglucomutase
4	52	22.8	137	T03488	glutamate-tRNA lig
5	52	22.8	433	C82713	polysaccharide bio
6	51.5	22.6	155	C86206	hypothetical prote
7	51	22.4	157	AG2775	protein-export mem
8	51	22.4	162	E97555	hypothetical prote
9	51	22.4	328	H81996	probable integral
10	51	22.4	328	E81225	hypothetical prote
11	51	22.4	317	T28826	hypothetical prote
12	51	22.4	814	JC7389	thyroid stimulat
13	51	22.4	1077	T20579	hypothetical prote
14	50.5	22.1	332	C64073	rbp repressor homo
15	50.5	22.1	425	E70813	hypothetical prote
16	50	21.9	168	S73450	MG027 homolog B01
17	50	21.9	231	F89856	conserved hypothet
18	50	21.9	281	B47629	cell surface glyco
19	50	21.9	685	T12139	NADH2 dehydrogenas
20	50	21.9	777	AC3273	cell division prot
21	50	21.9	1152	F86363	hypothetical prote
22	49.5	21.7	182	S40729	hypothetical prote
23	49	21.5	105	G71294	hypothetical prote
24	49	21.5	186	F86830	hypothetical prote
25	49	21.5	309	E71019	NADH2 dehydrogenas
26	49	21.5	309	H75113	NADH2 dehydrogenas
27	49	21.5	335	T16359	hypothetical prote
28	49	21.5	484	S36339	phosphorin II - V
29	49	21.5	488	T10794	phosphorin III -

30	49	21.5	599	2	T10798	phosphorin-S - Vo
31	49	21.5	619	2	AF2693	conserved hypothet
32	49	21.5	619	2	B97475	hypothetical prote
33	49	21.5	807	2	T40821	probable ubiquitin
34	49	21.5	1097	2	T40678	hypothetical prote
35	49	21.5	1299	2	A42090	two-component hybr
36	48.5	21.3	366	2	B86341	hypothetical prote
37	48.5	21.3	445	2	B82954	probable dihydroor
38	48.5	21.3	558	2	D59067	succinate dehydrog
39	48.5	21.3	747	2	H82943	hypothetical prote
40	48.5	21.3	1121	2	C87973	protein Y43F8C.12
41	48.5	21.3	1153	2	T26883	hypothetical prote
42	48.5	21.3	1695	2	J80084	voltage-gated sodi
43	48	21.1	227	2	E59101	hypothetical prote
44	48	21.1	260	2	A41531	TGFbeta-regulated
45	48	21.1	270	2	AF2008	permease protein o

ALIGNMENTS

RESULT 1

JC7903
collectin liver 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C;Accession: JC7903
R;Kawai, T.; Suzuki, Y.; Eda, S.; Kase, T.; Ohtani, K.; Sakai, Y.; Keshi, H.; Fukuh, A
Bioeci. Biotechnol. Biochem. 66, 2134-2145, 2002
A;Title: Molecular cloning of mouse collectin liver 1.
A;Reference number: JC7903; MUID:22333927; PMID:12450124
A;Accession: JC7903
A;Molecule type: mRNA
A;Residues: 1-277 <KAW>
A;Cross-references: DDBJ:AB016429
A;Experimental source: liver
C;Comment: This protein is a highly conserved cytosolic protein and belongs to a vertebr
c development.
C;Genetics:
A;Gene: C11
A;Map position: 15

Query Match 69.7%; Score 159; DB 2; Length 277;
Best Local Similarity 71.7%; Pred. No. 1.9e-14; Indels 0; Gaps 0;
Matches 33; Conservative 3; Mismatches 10; 13

QY	1	MNGFASLLRRNQFILLVFL	QIQSLGIDIDSRPTAEVCATHITSP	46
DB	1	MNGFVLLRSNLSMLLLALLH	FQSLGIDVDSRAAEVCATHITSP	46

RESULT 2

AE1996
hypothetical protein all1523 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1996
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1996
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA077889.1; PID:gl7135343; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1523

Query Match 23.2%; Score 53; DB 2; Length 386;